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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:18:50 1999; MasPar time 32.13 Seconds 686.752 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-08-866-354-38 (1-400) from US08866354.pep 3033 1 MVRPLNPRPLPPVVLMLLLL......PWVPSLFSCTLPLILLLSLW 400

Scoring table: PAM 150 Gap 11

Searched: 180763 segs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb18

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.106; Variance 78.006; scale 0.591

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2111554 21100 21187 21187	Result No.
3026 2358 2356 2356 711 701 700 701 701 701 701 701 681 681 681 113 113 113 113 113 113 113	Score
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7 4 014802 ACTIVIN TYPE I RECEPTO 1. 8 5 017966 C1481.9. 2. 8 6 002660 SCO-SPONDIN (FRAGMENT) 2. 9 5 015763 HYBRID HISTIDINE KINAS 2. 9 4 043612 PREPRO-OREXIN. 2. 1 4 043612 PREPRO-OREXIN. 3. 1 5 024900 EMMAREPLZ (FRAGMENT). 4. 1 10 006763 ADRII PROTEIN. 6. 8 6 062707 ENV PROTEIN. 6. 8 6 062707 ENV PROTEIN. 3. 1 10 02076 PHOSPHOLIPASE C BETA 3. 2 051338 PYOVERDINE SUNTHETASE 4. 1 11 062076 PHOSPHOLIPASE C BETA 3. 2 11 061271 ACTIVIN A RECEPTOR TYP 1. 2 5 077461 HEXAMERIN A (FRAGMENT) 1. 2 5 077461 HEXAMERIN A (FRAGMENT) 1. 2 5 0776210 HEXAMERIN A (FRAGMENT) 1. 2 5 077620 HEXAMERIN A (FRAGMENT) 1. 2 5 076209 HEXAMERIN A (FRAGMENT) 1. 2 5 076209 HEXAMERIN A (FRAGMENT) 1. 3 019346 FILC1. 5. 5 019346 FILC1. 5. 6 037429 NADH DEHYDROGENASE SUH 3. 8 037429 NADH DEHYDROGENASE SUH 3. 8 037582 NADH DEHYDROGENASE SUH 3. 8 037582 NADH DEHYDROGENASE SUH 3. 9 019582 NADH DEHYDROGENASE SUH 3.	4 4 U 4	4 4 4 4	4 4	4.	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
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	241 LPPVAPNCLELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM 300	Qy
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	181 AYGEACSGPHCQRHYCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240	Qy
	181 AYGEACSGPHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA 240	문
	121 HRARSLGNYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRK 180	Qy
	121 HRARSLGNYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRK 180	망
	61 YHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRUKUQVACLDIYWTV 120	Qy
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	1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAA 60	Qy
	1 MYRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAA 60	문
0:	Query Match 99.8%; Score 3026; DB 4; Length 400; Best Local Similarity 99.5%; Pred. No. 0.00e+00; Matches 398; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Quer Best Matc
	SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;	
	PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).	
	BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.;	RA E
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	HOMO SAPIENS (HUMAN). EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA: C.C.	
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O55243

PRELIMINARY; PRT; 397 AA.

O55243;

O1-JUN-1998 (TREMBLREL. 06, CREATED)

O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

O1-JUN-1998 (TREMBLREL. 06, LAST ANOTATION UPDATE)

GI-JUN-1998 (TREMBLREL. 06, LAST ANOTATION UPDATE)

GELAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY REC!

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GERAGOTA; MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EU'

SCIUROGNATHI; MURIDAE; MURINAE; MUS.
O35118 PRELIMINARY:
O35118; O1-JAN-1998 (TREMBLREL. 0
O1-JAN-1998 (TREMBLREL. 0
O1-NOV-1998 (TREMBLREL. 0
GLIAL CELL LINE DERIVED N
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GFRA3 OR GFRALPHA-3.
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NAVELIHAN P., BAUDET C., MIKAELS O., SHEN PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).

EMBL; AF041842; G2921579; -.

EMBL; AF036163; G2674177; -.

SEQUENCE 397 AA; 44302 MW; F77607CF CR
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Pred. No. 0.00e+00;
56; Mismatches 32;
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RESULT

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AC 035325

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DT 01-JAN-1998 (TREMBLREL 05

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DT 01-AUG-1998 (TREMBLREL 05

DE GLIAL CELL LINE-DERIVED NE

GN GFRA-3.

OS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDA

OC SCIUROGNATHI; MURIDAE; MUF

RN [1]

RP SEQUENCE FROM N.A.

RA TRUPP M., RAYNOSCHEK C., 1

RA TRUPP M., RAYNOSCHEK C., 1
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Best Local Similarity
Matches 306; Conser
SEQUENCE FROM N.A.

TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF020305; G2429367; -.

SEQUENCE 397 AA; 44333 MW; F0C0CB41 CI
                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; V
SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
EMBL; AB00883; D1024441; -.
EMBL; AF051766; G2961630; -.
EMBL; AF051766; G2961630; -.
MGD; MGI:1201403; GFRA3.
SEQUENCE 397 AA; 44307 MW; A80E0D24 CRC32;
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STRAIN-C57BL6; TISSUE-HEART;
STRAIN-C57BL6; TISSUE-HEART;
MEDLINE; 98205811.
NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
"Molecular cloning and expression analysis of GFR CDNA related to GDNER alpha and NYNR alpha.";
BIOCHEM. BIOPHYS. RES. COMMUN. 244:849-853(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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llarity 77.9%;
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5, LAST SEQUENCE UPDATE)
7, LAST ANNOTATION UPDATE)
7007ROPHIC FACTOR FAMILY R
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Pred. No. 0.00e+00;
53; Mismatches 31;
                                                                                                                                                                                          VERTEBRATA;
E; MUS.
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Query Match

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  Query Match
Best Local
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015507 PRELIMINARY;
01-JAN-1998 (TREMBLREL 0
01-JAN-1998 (TREMBLREL 0
01-JAN-1998 (TREMBLREL 0
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RETL1.
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PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";

PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
                                                                  SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; U997144; G2282026; -
EMBL; U99847; G2459742; -
SEQUENCE 460 AA; 50838 MW; 022FFECA CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SANICOLA M., HESSION C.A., WORLEY D.S., WALUS L., ROBINSON S., JAWORSKI G., WEI
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                         HISHIKI T., KONDOH K., ICHI
SAKIYAMA S., TAKAHASHI H.,
                                                                                                                                                                                                                                                                                                            SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EI
WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R.,
PEDINSKY R.B., CATE R.L.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATARRHINI; HOMINIDAE;
                                                                                                                                                                  NAKAGAWARA A.;
                                                                                                                                                                                                                                       EQUENCE FROM N.A.
ISSUE-SUBSTANTIA NIGRA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
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Similarity
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                                                                     022FFECA CRC32
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                                                                                                                                                                                         NIMURA Y., SI
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1.73e-137
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                      DB 4;
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Best Local Similarity
Matches 122; Conser
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                035252
                                                                                                                                                                                                                                                                                                                                   DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL, AF015172; G2624963;
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;
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01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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NEUROREPORT 9:0-0(0001).
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EVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC--RDVACTERRRQTIVPVCSYEEVERU ::
                                                                                                                                                                                                                                      LYFVLPLLDL-LMSAE-VSGGDRL-D-CVKASDQCLKEQSCSTKYRTLRQCVAGKETNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVA-VN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC--RDIACTERRRQTIVPVCSYEEREKFN
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                                          -- CQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCAL (1994)
                                                                                                                                                                                    LTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDLLEDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSSSLSVAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLELRRLCFSDPLCRSRLVDFQTHCHPMDI-LGTCATEQ-SRCLRAYLGLIGTAMTPNFA
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                                                                                                   YEDTVTSKPWKM--NLSKLNMLK-PDSDLCLKFAMLCTLNDKCDRLRKAYGEACS-G-PH
                                                                                                                                YE-PVNSRLSDIFRAVPFISVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTTSMSN 17:
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                                                                                                                                                           -SEEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYWTVHRARSLGNYELDVSP
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Pred. No. 4.81e-136;
73; Mismatches 128;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                       Length 463;
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035748;
01-JAN-1998
01-JAN-1998
01-JAN-1998
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O1-JAN-1998 (TREMBLREL 05, CREATED)
O1-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GDNFR-BETA OR RETL2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MANMALIA; EUTHER
                                                                                                                                                SEQUENCE FROM N.A.
TRUPP M., RAYNOSCHEK
SUBMITTED (JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)
GDNER-ALPHA/TRNR1-DELTA PROTEIN.
RATTUS NORVEGICUS (RAT).
EUKARYOTA, METAAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
SEQUENCE FROM N.A. TISSUE-BRAIN/KIDNEY; MEDLINE; 97322356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035977
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SUBMITTED (CCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;
                                                                                                                                                                                                                                                                                                        SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSPYEDTVTSKPWKM--NLSKLNMLK-PDSDLCLKFAMLCTLNDKCDRLRKAYGEACS-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLP-SEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNYELD 132
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l Similarity 34.8%;
120; Conservative
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Pred. No. 2.54e-135;
74; Mismatches 134;
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E; RATTUS.
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CVRANELCAAESNCSSRYRTLRQCLAG-RDR-NTMLAN--KECQAALEVLQESPLYDCRC 95

CLQARRKCQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMC

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DT 01-JAN-1998 (TREMBLREL 0:
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OS HOMO SAPIENS (HUMAN).
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OC EUKARYOTA; METAZOA; CHORDJ
OC CATARRHINI; HOMINIDAE; HON
RI [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FETAL BRAIN;
RA WARTIOVAARA K., SUVANTO P
RA MOSHNYAKOV M., AIRAKSINEN
RA MOSHNYAKOV M., AIRAKSINEN
RA SUBMITTED (MAR-1997) TO E
EMBL; U93703; G2228737; --
SQ SEQUENCE 464 AA; 51530
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Best Local (
                                                                                TISSUE-FETAL BRAIN;
WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL
MOSHNYAKOV M., AIRAKSINEN M.S., PALOTIE A., SARIOLA H., S
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U93703; G2228737; ...
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PEPINSKY R.B., CATE R.L.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF00526; G2232252;
EMBL; U97143; G2282024;
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                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
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SANICOLA M., HESSION C.A.,
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Local Similarity 35.3%;
les 121; Conservative
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 115;
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35.7%;
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR RECEPTOR
Score 701; DB 4; Le
Pred. No. 1.23e-133;
87; Mismatches 95;
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                                                                                                                                                                                                                             VERTEBRATA;
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H., TIZARD R.,
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ALIGNMENTS

RESULT

	CDS	gene ·		source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE	MEDLINE	JOURNAL	HITTE		AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION		DEFINITION	LOCUS
<pre>/gene="crn43" /note="GFRalpha3; GPI-linked receptor" /codon_start=1 /product="GDNF family receptor alpha 3" /db_xref="PID:92961632"</pre>	/gene="GFRA3" 1	/map="5931.2-q32" /map="5931.2-q32" 1	/Organism="Homo sapiens" /db_kref="twon:9606" /hromosome="f"		Location/Qualifiers	Submitted (03-MAR-1998) Pathology, Washington University, 660 South Euclid Ave, St. Louis, MO 63110, USA	Direct Submission	Gorodinsky, A., Fahrner, T.J., Baloh, R.H. and Milbrandt, J.D.	2 (bases 1 to 1203)	98245162	Proc. Natl. Acad. Sci. U.S.A. 95 (10), 5801-5806 (1998)	receptor family	Popescu, N.C., Johnson, E.M. Jr. and Milbrandt, J.	Baloh, R.H., Gorodinsky, A., Golden, J.P., Tansey, M.G., Keck, C.L.,	1 (bases 1 to 1203)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.		92961631	AF051767	cds.	iens GDNF family receptor alpha 3 (GFRA3)	AF051767 1203 bp mRNA PRI 26-JUN-1996

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
98205811
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Fax:81-52-736-5865)
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1 (bases 1 to 1884)
Baloh,R.H., Gorodinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L. Popescu,N.C., Johnson,E.M. Jr. and Milbrandt,J.

GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
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Mus musculus
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Baloh,R.H. and Milbrandt,J.D.
Direct Submission
Submitted (03-MAR-1998) Pathology,
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/db_xref-"PID:g2961630"
/translation-"MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLAir"
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Location/Qualifiers
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245 CTGATGTTGCTGCTGCTGCCGCCGCCGCCGCCGCCGCCCCCTT

95 CTGATGATCCTGCTACTGGTGCTGTCGTTGTGGCTGCCACTTGGAGCAGGAAACTCCCTT [5:]

Length 1911; Indels

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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1911)
Navellhan, P., Baudet, C., Mikaels, A., Shen, L., Westphal, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-NOV-1997) Lab.
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Naveilhan, P. and Ernfors, P.
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77, Sweden
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/family receptor alpha 3"
/db_xref="plD:g2674177"
/db_xref="plD:g2674177"
/translation="MGLSLEPREPLIMILLLVLSLWLPLGAGNSLATENRE V.S."
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RMKHQATCLDIWTVHPARSLGDYELDVSPYEDTVTSKPWKNNISKYLANT
KFAMLCTLHDKCDRLKKAYGEACSGIRCORHLCLAQLESFFEKALSST
PEDAGGGERRRWILAPSCALPSVTPNCLDLRSFGRADDLCRSFEKALSST
TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCKRSSRNI
RCLVCALAAKKRFHRQLFSQDWADSTFSVVQQQNSNPALRIGHSCHLST
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Zhong,J., Annies,M., Tolle,A. and Heumann, Molecular cloning of a new member of TrnR Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (14-OCT-1997) J. Zhong,
NC7/172, Ruhr-University Bochum, (
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                                                                                                          40.5%;
larity 82.1%;
Conservative
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/gene="firs-3"
/geneduct="TGF-beta-related neurotrophic receptor-3"
/product="TGF-beta-related neurotrophic receptor-3"
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DRIRKAYGEACSGIRCORHLCLAQLRSFFEKAAESHAQGLLLCPCPPEDAGCGFRREN
TIAPSCALESTYPNCLDIRSFCRADPLCRSTLADFOTHEMBDILGTCATEQSR:::\a\
TIAPSCALESTYPNCLDIRSFCRADPLCRSTLADFOTHEMBDILGTCATEQSR::\a\
TIGLIGTAMTPNFISKNMTTVALSCTCRGSGNLODECEDLERSFSQNPCLVEAIAARM
REHRQLESQDWADSTESVYQONSNPALRLQPRLPILSFSILPLILLQTLM"
R$66 C 491 g 441 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Swiss-Webster /N.
/db_xref="taxon:10990"
/dev_stage="15 days old"
/tissue_type="embryo"
118. 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              publication:
                                                                                                                                                                                                                                                                                                                                                                                                /gene="TrnR-3"
118. .1275
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Pred. No. 0.00e+00;
0; Mismatches 225;
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                                                                                          CTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGATGGCACACCAGAATGAAAAC
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Best Local Similarity 83.2%;
Matches 966; Conservative
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther!

Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1194)

Trupp, M., RaynosChek, C. and Ibanez, C.F.

Multiple GPI-anchored receptors control GDNF-dependent unit independent activation of the c-Ret receptor tyrosine kinds.

Oppublished
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Location/Qualifiers
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fdmily receptor alpha-3"
fdb_xref="pli-g2429567"
/translation="MGLSWSPRPPLIMILLLVLSLWLPLGAGNS: """
/translation="MGLSWSPRPPLIMILLLVLSLWLPLGAGNS: """
RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAUL_LLNSS
RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAUL_LLNSS
RWKHQATCLDIWTVHPARSLGDVELDVSDYEDTYTSKPWKMNLSKL.W...
REMALCTLHDKCDRLKAYGEACSGIRCQRHLCLAGLRSFERMADES[] | """
PEDAGCGERRRWITAPSCALPSVTPNCLDLRSFCRADPLCTSRLMDF9[] | """
PEDAGCGERRRWITAPSCALPSVTPNCLDLRSFCRADPLCTSRLMDF9[] | """
PEDAGCGERRAVIGHIGTAMTPNFISKVNTTVALSCTCRSGNLQDFCP, """
TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRSGNLQDFCP, """
RCLVEALAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSTS """
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/note-"structurally related to members of the CFRG
of GPI linked receptors for glial cell line derived
neurotrophic factor; GFRalpha-3"
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Submitted (07-JAN-1998) Neuroscience, Karolinska
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1 (bases 1 to 1244)
Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and GFRalpha-3, a protein related to GFRalpha-1, is expideveloping peripheral neurons and ensheathing cells Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
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         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 521)

Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hiller, L., Wilson, R. and Waterston, R.
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 521)
AUTHORS Waterston, R.

Direct Submission
Direct Submission
University, 4444 Forest Park Avenue, St. Louis, Missouri Park
SUBMITTED BY:
SUBMITED BY:
SUBMITTED BY:
SUBMITTED BY:
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ORIGIN 밁 FEATURES Query Match 23.4%; Best Local Similarity 99.6%; Matches 468; Conservative COUNT source 41 GGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTCCAGTCCTCATTCCCTCCACC 100 ø /Organism "Homo sapiens"
/db_xref="taxon:9606"
/clone_lib-"Soares_fetal_heart_NbHH19W"
/clone="IMAGE:343930"
147 c 120 g 143 t Score 466; DB 27; Pred. No. 0.00e+00; 0 Mismatches Length 521; Indels 0 Gaps

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Local Similarity 97.18;
                         TTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAAACCTTTGACTT 511
                                                                                             GGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCTGTGGGCCTTGCTTTATTCCTA 55
                                                                                                                                              GGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCTGTGGGCCTTTGCTTATTCCTA 458
                                                                                                                                                                                                CCCCTCG-CTCCTCCCCTGGATGGAGGATGGAAAACTACTGCCTGCACTGCCCTGTCCCC 115
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FLI_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
Submitted (24-AUG-1998) Department of Genetics, Wissouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chapper, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hillier, L., Wilson, R. and Waterston, R.
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Department of Genetics
Washington University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         St. Louis MO 63108, USA http://genome.wustl.edu/gscmailto:est@watson.wustl.edu
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/db_xref="taxon:9606"
/clone_lib="Soares_fetal_heart_NbHH19W"
/clone="IMAGE:343930"
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Pred. No. 2.82e-97
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GFRalpha-3.
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166494
                                     Submitted (13-NOV-1997) to the DDBJ/EMBL/GenBank databases. Sate Nomoto, RIXEN (The Institute of Physical and Chemical Research), Bio-Mimette Control Research Center: 2271-130 Anagahora, Shimoshidami, Moriyama-ku, Nagoya, Alchi 463, Japan
            (E-mail:nomoto@nagoya.riken.go.jp, Fax:81-52-736-5865)
                                                                                                  Direct Submission
                                                                                                                                         9820581
                                                                                                                                                        Nomoto,S., Ito,S., Yang,L.X. and Kiuchi,K.
Molecular cloning and expression analysis of GFR alpha-3,
CDNA related to GOMERR alpha and NTNR alpha
Biochem. Biophys. Res. Commun. 244 (3), 849-853 (1998)
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                     Mus musculus
AB008833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997;
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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llarity 0.9%;
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1491 c 1486 g
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1. .7218
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Pred. No.
209; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1884)

Baloh,R.H., Gorodinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L.
Popescu,N.C., Johnson,E.M. Jr. and Milbrandt,J.

GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
                                                                                                                                                                                                                           Submitted (03-MAR-1998) Pathology, Washington University, 660 South Euclid Ave, St. Louis, MO 63110, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1884)
Baloh, R.H. and Milbrandt, J.D.
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AF051766
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larity 76.5%;
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/product="GDNF family receptor alpha 3"
/db_xref="PID:92961630"
/translation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENREVNSCTQA
RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
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KFAMLCTLHDKCDTARSKYGEACSGIRCQRHLCLAQLRSFEKAAESHAGGLLLCPCA
PEDAGCGERRRNTIARSKALPSVPRCLDLRSFCRADPLCFSRLMDFCTHCHPWDLL
TCATEOSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
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/db_xref="PID:3d1024441"
/db_xref="PID:3d27160"
/translation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
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/strain="C57BL6"
                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                    /note="GFRalpha3; GPI-linked receptor; r
(GDNFRa, TRNR1, RETL1) and GFRa2 (TRNR2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
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/dev_stage="adult"
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family receptor alpha 3 mRNA,
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Pred. No. 3.50e-16;
0; Mismatches 23
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-OCT-1997) J. Zhong,
                                                                                                                                                                                                                                                                                                                                                                                                                  L, Zhong
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Molecular cloning of a
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Similarity 76.58;
75; Conservation
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PEDAGCGERRRNTIAPSCALFSVTPNCLDLRSFCRADPLCRSRLMDFOTHCHPWDILD
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                                                                                                                                                                                                                                                                   /strain="Swiss-Webster
/db_xref="taxon:10000"
/dev_stage="15 days old
                                                                                                                                                                                                                                        /tissue_type="embryo"
| 118. .162
                                                                                                                                                                           /gene="TrnR-3"
                                                                                                                                                                                                                            'gene-"TrnR-3"
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Pred. No.
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Mus.
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Query Match Best Local Similarity

2.6%;

Score Pred.

No.

DB 29; ; 3.50e-16;

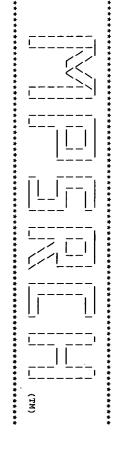
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DEFINITION
ACCESSION
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Mus musculus glial cell line-derived neurotrophic
receptor alpha 3 (gfra3) mRNA, complete cds.
AF036163
g2674176
                                                                                               Submitted (28-NOV-1997) Lab. Mol. Neuro. Dept. Medical Biochemistry and Biophysics, Karolinska Institute, Doktorsringen 12A, Stockholm 171 77, Sweden
                                                                                                                                                                                                                                                                           Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1911)
1 (bases 1 to 1911)
Naveilhan, P., Baudet, C., Mikaels, A., Shen, L., Westphal, H. and Naveilhan, P., Baudet, C., Mikaels, A., Shen, L., Westphal, H. and
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Sequence 14 from patent US 5670367.
166494
                                                                                                                                                                                                             Expression and regulation of GFRalpha3, a glial cell line-derived neurotrophic factor family receptor Proc. Natl. Acad. Sci. U.S.A. 95 (3), 1295-1300 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Naveilhan, P. and Ernfors, P.
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                                /organism="Mus musculus"
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/gene="gfra3"
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44 A-AAGTCTCTCTGGGCTCTTGGATCATGATTAAACCTTT
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/gene="gfra3"
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Search completed: Fri Mar 12 03:17:36 1999 Job time : 6561 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Fr1 Mar 12 11:35:08 1999; MasPar time 2954.55 Seconds 1358.935 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-866-354-41 (1-1699) from US08866354.seq 1699

N.A. Sequence: Comp: 1699

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Scoring table: TABLE default Gap 6

Dbase 0; Query 0

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STD :

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_v1 9enbank110

Database:

16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 25:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi

Statistics: Mean 11.296; Variance 5.216; scale 2.166

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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110 110 111 112 113	Result
1128 1126 1125 1125 1038 1027 764 41 41 37 37	Score
46666666666666666666666666666666666666	Query Match
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ALIGNMENTS

	CDS	FEATURES source	TITLE JOURNAL	REFERENCE	JOURNAL MEDLINE	TITLE	REFERENCE	KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION ACCESSION NID
/note="GFRalpha3; GPI-linked receptor; related to GFRal (GDNFRa, TRNR1, RETL1) and GFRa2 (TRNR2, NTNRa, RETL2)" /codon_start=1 /codon_start=1 /product="GDNF family receptor alpha 3" /product="GDNF family receptor alpha 3" /db_xref="pID:92961030" /translation="MGLSWSPRPLMILLIVISLMLPLGAGNSLATENREVNS:1::" / rkkceanpackaay0HLGSCTSSLSRPLPLEESAMSADCLEAAEQLENSS!!NY::" Rkkceanpackaay0HLGSCTSSLSRPLPLEESAMSADCLEAAEQLENSS!!NY::" Rkkceanpackaay0HLGSCTSCLDVSPYEDTYTSKPWKMLSKLNNLKPINS!		11884	Direct Submission Submitted (03-MAR-1998) Pathology, Washington University, 660 South	2 (bases 1 to 1884) Baloh,R.H. and Milbrandt,J.D.	receptor family Proc. Natl. Acad. Sci. U.S.A. 95 (10), 5801-5806 (1998) 98245162	Popescu, N.C., Johnson, E.M. Jr. and Milbrandt, J. GFRalpha3 is an orphan member of the GDNF/neurturin/persephin	Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1884) Baloh,R.H., Gorodinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L.,	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;	AF051766 1884 bp mRNA ROD 26-JUN-1998 Mus musculus GDNF family receptor alpha 3 mRNA, complete cds. AF051766 g2961629

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Submitted (14-OCT-1997) J. Zhong, Molecular Neurobiochemistry
Submitted (14-OCT-1997) J. Zhong, Molecular Neurobiochemistry
NC7/172, Ruhr-University Bochum, Universitaetsstr. 150, D-44780
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/product="ToF beta-related neurotrophic receptor-3"
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118. .162
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Mus musculus I
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GFRalpha-3.
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Submitted (13-NOV-1997) to the DDBJ/EMBL/GenBank database.
Nomoto, RIKEN (The Institute of Physical and Chemical Resembler-Mimetic Control Research Center; 2271-130 Anagahora, Shimoshidami, Moriyama-ku, Nagoya, Aichi 463, Japan (E-mail:nomoto@nagoya.riken.go.jp, Tel:81-52-736-5864, Fax:81-52-736-5865)
                                                                                                                                                                                                                                                                                                                                                                                                               Nomoto,S., Ito,S., Yang,L.X. and Kiuchi,K. Molecular cloning and expression analysis cDNA related to GDNFR alpha and NTNR alpha
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Naveilhan, P. and Ernfors, P.
Direct Submission
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Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 1911)
Naveilhan, P., Baudet, C., Mikaels, A., Shen,
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/function="gDNF |
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/product="glial cell line-derived neurotrophic factor family receptor alpha 3"
/db_xref="piD:g267417".
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Mus musculus glial cell line-derived neurotrophic
receptor alpha-3 (gfra3) mRNA, complete cds.
AF041842
g2921578
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Submitted (07-JAN-1998) Neuroscience,
Doktorsringen 12, Stockholm 17171, Swe
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1 (bases 1 to 1244)
Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and GFRalpha-3, a protein related to GFRalpha-1, is expr developing peripheral neurons and ensheathing cells Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
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/gehe="gfra3"
/gehe="gfra3"; similar to GFRalpha-1; expressed in developing peripheral nervous system"
/codon_start=1
/codon_start=1
/product="glial cell line-derived neurotrophic factor family receptor alpha-3"
/db_xref="plD:g2921579"
/db_xref="plD:g2921579"
RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKNNLSKLNMLKPDSDLC:L
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Doktorsringen 12A, Stockholm 17177, Sweden
Location/Qualifiers
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/trans1ation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENREVNSCTQA
/trans1ation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENREVNSCTQA
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RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNNLKPDSDL/CL
KFAMLCTLHDKCDRLKKAYGEACSGIRCQRHLCLAQLRSFERAAESHAQGLLLCPCP
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PEDAGCERRRNTIAPSCALPSVTPNCLDLTSFCRADFLOTGRSKNLODECGLERSFSQ
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TCATEGSRCLAAYIGLIGTAWTPNF15KVNTTVALSCTCRGSGNLODECGLERSFSQ
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/note-"structurally related to members
of GPI linked receptors for glial cell
neurotrophic factor; GFRalpha-3"
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1 (bases 1 to 1203)

Baloh, R. H., Gorodinsky, A., Golden, J. P., Tansey, M.G., Keck, C. L. Popescu, N.C., Johnson, E. M. Jr. and Milbrandt, J. GFRalpha3 is an orphan member of the GDNF/neurturin/persephin receptor family
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Submitted (03-MAR-1998) Pathology, Washington Co. 10118, MO 63110, USA
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/db_xref="piD:g2961632"
/translation="MVRPLNPRPLPPVLMLLLLLPPSPLPLAAGDPLPTESKLMNS"
LQARRKCQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLENES"
CHRKHNQVACLDIYMTVHRAASLGNYELDVSFYEDTVTSKPMKNNLKKLNSLKL
LCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQLLTFFEKAAFFHAN
PCAPNURGCGERRRNTIAPNCALPPVAPNCLELRRLCFSDPLCRSRLYN
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/note="GFRalpha3; GPI-linked receptor"
/codon_start=1
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/db_xref="taxon:9606"
/chromosome="5"
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I66494 Sequence 14

7218 bp DNA from patent US

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128278
g1819054
                                                                                Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
1. .215
                                                                                                                 1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H
Plant inhibitors of fungal polygalacturonases and
control fungal disease
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33; Conservative
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14_23-SEP-1997;
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Score 41; DB 22; Le
Pred. No. 2.06e-10;
86; Mismatches 90;
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(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Mar 8 14:41:49 1999; MasPar time 14.57 Seconds 731.149 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence:

>US-08-866-354-42 (1-397) from US08866354.pep 2962 1 MGLSRSPRPPPLVILLLVLS.....LRLPVLSFFILTLILLQTLW 397

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 l:swissprot

Statistics: Mean 47.465; Variance 72.568; scale 0.654

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult	Score	% Query Match	Length	BB	IJ	Description	Pred. No.
1	788	6	465	_ ;	NRTR_CHICK	NEURTURIN RECEPTOR ALP	1.13e-170
2	762	25.7	463	μ	NRTR_MOUSE	EPTOR	1.00e-163
ω	759	25.6	464	ب	NRTR_HUMAN		6.34e-163
4	749	25.3	469	ب	GDNR_CHICK	GDNF RECEPTOR ALPHA PR	2.95e-160
u	708		468	ـــ	GDNR_MOUSE	GDNF RECEPTOR ALPHA PR	2.42e-149
σ	695	23.5	468	 -	GDNR_RAT	GDNF RECEPTOR ALPHA PR	.84e-
7	694	23.4	464	44	GDNR_HUMAN	RECEPTOR ALPHA	
œ	115	3.9	345	μ,	GAS1_HUMAN	771	2.00e-04
9	115	3.9	384	۳	GAS1_MOUSE	GROWTH-ARREST-SPECIFIC	2.00e-04
10	104	3.5	354	۳	ADA_ECOLI	ADA REGULATORY PROTEIN	1.39e-02
11	102	3.4	381	_	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	2.92e-02
12	102	3.4	459	_	IL7R_HUMAN	INTERLEUKIN-7 RECEPTOR	2.92e-02
13	97	ω .ω	875	سا	ENV_BIV06	ENV POLYPROTEIN PRECUR	1.76e-01
14	97	ω. ω	904	μ	ENV_BIV27	ENV POLYPROTEIN PRECUR	1.76e-01
15	98	ω .ω	1655	<u>_</u>	N188_YEAST	NUCLEOPORIN NUP188 (NU	1.24e-01.
16	95	3.2	352	\vdash	ADA_SALTY	ADA REGULATORY PROTEIN	3.55e-01
17	94	3.2	391	_	BRB2_HUMAN	B2 BRADYKININ RECEPTOR	5.01e-01
18	95	3.2	519	_	NIFL_AZOVI	NITROGEN FIXATION REGU	3.55e-01
19	94	3.2	692	μ	HEXA_ANOGA	HEXAMERIN 1.1 PRECURSO	5.01e-01
20	91	3.1	235	μ	VIF_SIVAT	VIRION INFECTIVITY FAC	1.39e+00
21	93	3. <u>1</u>	410	_	CPXY_BACSU	CYTOCHROME P450 (EC 1.	7.06e-01
22	93	3.1	755	Н	YCJT_ECOLI	HYPOTHETICAL 84.9 KD P	7.06e-01
23	90	3.0	64	_	LAP_BOVIN	LINGUAL ANTIMICROBIAL	1.93e+00

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HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
JOHNSON E.M. JR., MILBRANDT J.;
NEURON 18.793-802(1997).
-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (TG:
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97325791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFRA2 OR GDNFRB OR TRNR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        008842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRTR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GDNFR-BETA)
    4
                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE GDNFR FAMILY.
L; AF002701; G2145082; -.
; MGI:1195462; GFRA2.
EPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).

TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN AND IN THE ADRENAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CTQARKKCEANPACKAAYQHLDSCTPSLSSPLPSGESATSAACLEAAQQLRNSSLIDCRC
                                       CVRANELCAAESNCSSRYRTLRQC---LAGR-DRNTMLANKECQAALEVLQESPLYDCRC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNLQDECEQLEKSFSQNPCLMEAIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNLEEECEKFLRDFTENPCLRNAIQA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADFHANCQASFQSLTSCPGDNYQACLGSYTGLIGFDMTPNYVDASTTSITISPWCSCKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KP--DS--DLCLKFAMLCTLNDKCDRLRKAYGEACS-GI----RCQRHLCLAQLRSFFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDFQTHCHP-MDILGTCATEOSR-CLRAYLGLIGTAMTPNFISKVNTTVALG--CTCRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVA-PNCLDLRSFCRADPLCRSRL
                                                                                             122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           SPLICING.
                                                                                                                                                                                                                                                                                                                                                           444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                   25.78;
                                                                                                                                                                                                                443
146
                                                                                                                                                                                                                                                                                                                                                           463
                                                                                                                                                                                                                                                                                                                                                                                                       443
                                                                                                                                                                                          51598
                                                                                                                                                                                          MW.
                                                                                             Score 762; DB 1; L
Pred. No. 1.00e-163;
75; Mismatches 100;
                                                                                                                                                                                                                                                                               HYDROPHOBIC,
(POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                     POTENTIAL.

GPI-ANCHOR (POTENTIAL).

MISSING (IN SHORT FORM).

; 0A2165C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                               TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                             Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                      REMOVED
                                                                                                                                      Length 463;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                      DURING
                                                                                                                                                                                                                                                                                                                                                      MATURATION
                                                                                          25;
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100
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    Query Match
Best Local S
Matches 12
                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRTR_HUMAN STANDARD; PRT; 464 AA.
000451;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
                                                                                            SEQUENCE
                                                                                                              VARSPLIC
                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR.
-!- SUBCELLULAR LOCATION:
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
JOHNSON E.M. JR., MILBRANDT J.;
NEURON 18.793-802 (1997).
-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 97325791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFRA2 OR GDNFRB OR TRNR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNFR-BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
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                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED SPLICING IN BOTH BRAIN AND PLACENTA.
SIMILARITY: BELONGS TO THE GDNFR FAMILY.
L; AF002700; G2145080; -.
                                                                                                                                                                                                                                                                                                                                                                           601956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECEQLEKSFSQNPCLMEAIAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THCHPM-DILGTCATEQSR-CLRAYLGLIGTAMTPNFISKVNTTVALG--CTCRGSGNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRRMKHQATCLDIYWTVHPVRSLGDYEL-DVSPYEDTVT--SKPWKM-NL-S-K-L-SHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRGMKKELQCLQIYWSIHLGLTEGE-EFYEASPYEPVTSRLSDIFRLASIFSGTGADPVV 154
  ch 25.6%;
l Similarity 37.3%;
120; Conservative
                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN;
                                                                                            464 AA;
                                                                                                                                                        52
357
413
                                                                                                                                                                                                                                              445
                                                                                                                                                                                                                                                                                                                              SPLICING
                                               52
3 441
441
146
51558 MW;
                                                                                                                                                                                                                                              464
                                                                                                                                                                                                                                                                                      444
                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                   GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACHED TO THE MEMBRANE
                                                                                POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

GPI-ANCHOR (POTENTIAL).

MISSING (IN SHORT FORM)

3C74BBFB CRC32;
  Score
Pred.
78; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344
                                                                                                                                                                                                                                                           POTENTIAL.
TGF-BETA R
RECEPTOR 2
                                                                                                                                                                                                                   HYDROPHOBIC, (POTENTIAL).
re 759; DB 1; Le
1. No. 6.34e-163;
Mismatches 99;
                                                                                                                                                                                                                                                                                    RELATED NEUROTROPHIC FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAPODA;
                                                                                                                                                                                                                                       REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                           FORM)
                                          Length
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΥВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAMMALIA
                                            464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A GPI-ANCHOR
  25;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
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  18:
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CVRANELCAAESNCSSRYRTLRQC---LAGR-DRNTMLANKECQAALEVLQESPLYDCRC

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2. 我是我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我	

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****	(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:07:03 1999; MasPar time 36.88 Seconds 694.165 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-866-354-36 (1-464) from US08866354.pep 3386 1 MILANVECLEFELDDTLRSL.....RARPSAALTVLSVLMLKLAL 464

Scoring table: PAM 150 Gap 11

Searched: 180763 segs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb18

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.920; Variance 70.591; scale 0.665

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 20			_							6 0					ω	2	<u></u>	Result No. So
101 98	103	102	110	107	705	782	782	782	1392	1499	1508	1520	1527	1535	3232	3365	3383	A excos
νω 00	ω (Ο F		ນ ເມ ນ (V	3.2		23.1	23.1		41.1		44.5	44.9	45.1	45.3	95.5	99.4	99.9	% Query Match L
483	287	193	2090							460			468	463	464	464	464	Length
10	4 (лu	n U	1	4	11	11	11	13	4	11	4	11	H	H	4	4	DB
082704	076101	001471	094247	088349	060609	055243	035325	035118	093512	015507	035252	043912	035246	035748	035977	015316	015328	ID
1-CYCLOPROPANE-1-CARBO	CD97_HUMAN, PARTIAL CD	CODED FOR BY C. ELEGAN	FOR BY C.	LATENT TGF BETA BINDIN	GDNF FAMILY RECEPTOR A	CELL	GLIAL CELL LINE-DERIVE	GLIAL CELL LINE DERIVE	GFR RECEPTOR ALPHA 4 P	RET LIGAND 1.	GDNF RECEPTOR BETA.	GPI-LINKED ANCHOR PROT	GDNF RECEPTOR ALPHA.	GDNFR-ALPHA/TRNR1-DELT	GLIAL CELL LINE-DERIVE	GLIAL CELL LINE-DERIVE	RET LIGAND 2.	Description
6.32e-02	2.98e-02	1 396-03	1.98e-03	6.41e-03	5.00e-151	6.73e-172	6.73e-172	6.73e-172	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.

			_	0	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
92 91	93	91	92	92	91	93	92	90	91	92	94	96	94	96	95	96	95	99	98	99	99	98	98
2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2 8	8	2 8					2.9				2.9	
1732 2404	1544	939	686	686			474	469	179	165	4131	939	482	344	338	201		4472				179	165
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MYTONIC DYSTROPHY KINA POLYPROTEIN.	SIMILAR TO DROSOPHILA	STRAIN 7G8 CG9 (CG9) A	MASP-2.	MASP-2 PROTEIN.	B0212.1 PROTEIN.	1-AMINOCYCLOPROPANE-1-	1-AMINOCYCLOPROPANE-1-	THIOLASE.	F52H3.5.	HYPOTHETICAL 17.7 KD P	F18C12.1.	STRAIN DD2 HEAT SHOCK	ACC SYNTHASE.	DCIAE PROTEIN.	HUPU AND HUPV GENES, C	TRANSCRIPTIONAL REGULA	HYPOTHETICAL 17.7 KD F	TYLACTONE SYNTHASE STA	F26A3.6.	1-AMINOCYCLOPROPANE-1-	ACC SYNTHASE (EC 4.4.1	19.7 KDA PROTEIN.	HYPOTHETICAL 17.8 KD P
1.61e+00 2.28e+00	1.14e+00	2.28e+00	1.61e+00	1.61e+00	2.28e+00	1.14e+00	1.61e+00	3.20e-00	2.28e+00	1.610.00	8.020-01	3.940.0.	8.020 (1		5.6.		'n	:•		•	:-	:	

ALIGNMENTS

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181 YISICNREISPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERHK()" 1917;	181 YISICNREISPTERCNRRKCHKALROFFDRVPSEYTYRMLFCSCODOACASH	121 EFYEASPYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNUN NOON	121 EFYEASPYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDWTKTT	61 ROCLAGRORNTMLANKECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWS1HL; -: -:	61 ROCLAGRORNIMLANKECQAALEVLQESPLYDCRCKRGMKKELQCLQIYMSIHI (**) ? * '!	1 MILANVECLEFELDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAESNCSSKYKII.	1 MILANVFCLFFFLDETLRSLASPSSLOGPELHGWRPPVDCVRANELCAAESNCSSRYRTI.	Query Match 99.9%; Score 3383; DB 4; Length 464; Best Local Similarity 99.6%; Pred. No. 0.00e+00; Matches 462; Conservative 2; Mismatches 0; Indels 0; Gaps 11;	SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;	TOTAL COLORS OF THE TAXABLE CANADA CA	PROC. NATE. ACAD. SCT. H.S.A. 94.6238-6243/1997)	"Gilal cell line-derived neurotrophic factor-dependent RET activation	PEPINSKY R.B., CATE R.L.;	H., TIZARD R.	SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,	MEDLINE; 97322356.	TISSUE-LIVER:	SEOUENCE FROM N.A.	CATARRHINI; HOMINIDAE; HOMO.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;		RETL2.		(TREMBLREL. 08,	(TREMBLREL. 05,	01-JAN-1998 (TREMBLREL: 05, CREATED)	O10306 FRELIMINARI; FRI; 404 AA.	

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ID 315316;
AC 015316;
AC 015316;
AC 015316;
DT 01-JAN-1998;
DT 01-JAN-1998;
DT 01-AUG-1998;
DE GLIAL CELL L.
GN GDNFR-BETA.
OS HOMO SAPIENS
OC CATARRHINI;
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RC TISSUE-FETAL
RA WARTIOVAARA IN
RA WARTIOVAARA IN
RA SUBMITTED (MI
DR EMBL; U93703;
SO SEQUENCE 40
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Matches 46
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EUKARYOTA, METAZOA; CHORDATA: V. CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL MOSHNYAKOV M., AIRAKSINEN M.S., PALOTIE A., SARIOLA H., S
SUBMITTED (MAR-197) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U93703; G2228737; -
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CFTELTINIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLKQAL
                                                     VNVSPKGPSFQATQAPRVEKTPSLPDDLSDSTSLGTSVITTCTSVQEQGLKANNSKELSM
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1 Similarity 99.1%;
460; Conservative
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3365; DB Pred. No. 0.00e+ 2; Mismatches
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035977;
035977;
01-JAN-1998
01-JAN-1998
01-NOV-1998
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SANICOLA M., HESSION C.A., WORLEY D.S., CA
WALUS L., ROBINSON S., JAWORSKI G., WEI H.
PEPINSKY R.B., CATE R.L.;
SUBMITED (APR-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF00526; G2232252;
EMBL; BF00526; G2282024;
EMBL; U97143; G2282024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLIAL CELL LINE-DERIVED NEUROI
GDNFR-BETA OR RETL2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
SCIUROGNATHI; MURIDAE; MURINAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., « PEPINSKY R.B., CATE R.L.; REPINSKY R.B., CATE R.L.; "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins."; PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-BRAIN/KIDNEY; MEDLINE; 97322356.
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                                                                                        VNVSPKGPSFQATQAPRVEKTPSLPDDLSDSTSLGTSVITTCTSVQEQGLKANNSKELSH
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l similarity 94.2%;
437; Conservative
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05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR RECEPTOR-BETA.
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Pred. No. 0.00e+00;
18; Mismatches 9;
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E; RATTUS.
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H., TIZARD R
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) 035748

; 035748;

1 01-JAN-1998 (TREMBLREL. 05, CREATED)

I 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDAT

I 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPI

GONER-ALPHA/TRNR1-DELTA PROTEIN.

S RATTUS NORVEGICUS (RAT).

S RATTUS NORVEGICUS (RAT).

C EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMM

C EUKARYOTA; METAZOA; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 22
                                                                                                                        SULT 5

O35246; PRELIMINARY; PRT
O35246; O1-JAN-1998 (TREMBLREL. 05, CREAT
O1-JAN-1998 (TREMBLREL. 05, LAST
O1-JAN-1998 (TREMBLREL. 05, LAST
O1-JAN-1998 (TREMBLREL. 05, LAST
GDNF RECEPTOR ALPHA.
GDNFR-ALPHA.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VER
SCIUROGNATHI; MURIDAE; MURINAE; M
SEQUENCE FROM N.A.
STRAIN-CS7: TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO H
NEUROREPORT 9:0-0(0001).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-HANNOVER;
ZHONG J., ANNIES M., HEUMANN R.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSDFGKDGLAGASSHITTKS-MA-APPSCSLSSLPVLMLTALA 452
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llarity 48.4%;
Conservative
                                             H.P.;
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; Pred. No. 0.00e+00;
101; Mismatches 115
                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                     VERTEBRATA;
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                                                                                                                                                     EUTHERIA;
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RESULT
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Best Local S
Matches 21
TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
SHEFELBINE S.E., KHORANA S., SCHULTZ P.N., HU
FOX G.M., JING S., COTE G.J., GAGEL R.F.;
HUM. GENET. 0:0-0(1998).
EMBL; AF038412; G2921545; JOINED.
EMBL; AF038411; G2921545; JOINED.
EMBL; AF038413; G2921545; JOINED.
EMBL; AF038414; G2921545; JOINED.
EMBL; AF038414; G2921545; JOINED.
EMBL; AF038414; G2921545; JOINED.
EMBL; AF038415; G2921545; JOINED.
EMBL; AF038416; G2921545; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SULT 6
043912;
043912;
01-TUN-1998 (TREMBLREL 06, C
01-TUN-1998 (TREMBLREL 06, C
01-AUG-1998 (TREMBLREL 07, I
01-AUG-1998 (TREMBLREL 07, I
GPI-LINKED ANCHOR PROTEIN.
GFRA1.
                                                                                                                                                                                                                                                       GENOMICS
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STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF014117; G2624961; ...
SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CH
                                                                                                                                                                                                                                                                      ANGRIST M., JING S., I
FOX G.M., CHAKRAVARTI
GENOMICS 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                               CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKALRQFFDKVPAKHSYGMLFCSCRDVACTERRRQTIVPVCSYEERERPNCLNLQDSCKJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFTE--LTTNIlFKSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDNDYGKDGLNGAGE
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                                                                                                                                                                                                                                                                                                                                                                               HOMINIDAE;
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llarity 48.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                   BOLK
                                                                                                                                                                                                                                                                                                                                                                               HOMO
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; Pred. No. 0.00e+00;
104; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQ
LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                                                                                                   BENTLEY
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ANNOTATION
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035252; OTREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
GDNF RECEPTOR BETA.
                                       SEQUENCE FROM N.A. STRAIN=C57; DEY B.K., WONG Y.W. NEUROREPORT 9:0-0(0
                                                                                                                                                                 GDNFR-BETA.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
SCIUROGNATHI; MURIDAE; MURINAI
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SEQUENCE FROM N.A.
STRAIN-C57;
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3L: AF038418; G2921545; JOINED.
3L: AF038419; G2921545; JOINED.
3L: AF038421; G2921532; -.
3L: AF038421; G2921532; -.
3L: AF058999; G3068783; JOINED.
3L: AF058999; G3068783; JOINED.
3L: AF058991; G3068783; JOINED.
3L: AF058992; G3068783; JOINED.
3L: AF058992; G3068783; JOINED.
3L: AF058993; G3068783; JOINED.
3L: AF058994; G3068783; JOINED.
3L: AF058995; G3068783; JOINED.
3L: AF058995; G3068783; JOINED.
3L: AF058997; G3068783; JOINED.
3L: AF058997; G3068783; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCT
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                                                                WONG Y.W., TOO
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llarity 48.1%;
Conservative
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Pred. No. 0.00e+00;
101; Mismatches 122;
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LAST ANN
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ANNOTATION UPDATE)
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                                                                                                                                                                                                 RODENTIA;
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RESULT

AC 015507

AC 01-JAN-1998 (
DT 01-JAN-1998 (
AC 01-JAN-1998 (
AC 01-JAN-1998 (
AC RETLIA

OS HOMO SAPIENS

OC EUKARYOTA; ME

OC CATARRHINI; H

RN [1]

RP SEQUENCE FROM

RC TISSUE-KIDNEY

RX MALUS L., ROE

RA MALUS L., ROE

RA PEPINSKY R.B.

RT G11A1 Cell 1

RT Can be mediat

RL PROC. NATL. A

RN [2]

RP SEQUENCE FROM

RC TISSUE-KIDNEY

RA WALUS L., ROE

RA WALUS L. ARI

RA SEQUENCE FROM

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RN SEQUENCE FROM

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Best Local
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MEDLINE; 9732336.

MEDLINE; 9732336.

SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLE C.,
SANICOLA M., HESSION S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.
WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.
PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activation."

"Glial cell line-derived neurotrophic factor-dependent RET activation.
"Glial cell line-derived neurotrophic factor-dependent RET activation.

"Glial cell line-derived neurotrophic factor-dependent RET activation."

"Glial cell line-derived neurotrophic factor-dependent RET activation."

"Glial cell line-derived neurotrophic factor-dependent RET activation."
                                                                             WALUS L., ROBINSON C.A., WORLEY D
WALUS L., ROBINSON S., JAWORSKI G.,
PEPINSKY R.B., CATE R.L.,
SUBMITTED (APR-1997) TO EMBL/GENBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/C
EMBL; AF015172; G2624963; -.
SEQUENCE 463 AA; 51134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
         SEQUENCE FROM N.A.
TISSUE-SUBSTANTIA NIGRA;
                                                                                                                                                                         TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| : | || :|: |:|::: ||
436 VIKPNSGPSRARPSAALTVLSVLMLK-LA
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| ::|: | :||::| | | | ||::|
26 LQGPELHGWRPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
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3 (TREMBLREL.
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                                                                             EMBL/GENBANK/DDBJ
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; Pred. No. 0.00e+00;
103; M1smatches 106;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; MAMMALIA; EUTHERIA: PRIMARES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                         CARMILLO P., E
H., TIZARD R.,
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                                           Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                           O93512 PRELIMINARX;
O93512;
O93512;
O1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GFR RECEPTOR ALPHA 4 PRECURSOR.
GALLUS (CHICKEN).
GALLUS GALLUS (CHICKEN).
EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
                                                                                                                                                                              SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISHIKI T
                                                                                                                                                                                                 WYATT S., BUCHMAN V.L., DAVIES A.M.;
"GFRALIPha-4, a new GDNF family receptor.";
MOL. CELL. NEUROSCI. 11:117-126(1998).
EMBL; AF045162; G2906032; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (OCT-1997) TO EMBL; U97144; G2282026; EMBL; U95847; G2459742; SEQUENCE 460 AA; 5083
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 98313402.
                                                                                                                                                                                                                                                                                                               MEDLINE; 98313402.
THOMPSON J., DOXAKIS E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKAGAWARA A.;
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSVS-NDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEER 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGNYEKEGLGASSHITTKS-MA-APPSCGLSPLLVLVVVT-AL: | : | : | | | | : | | | : | | | : | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFPVQTTTATTTTALRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLCIS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNYIDSS-S-LSVAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGSDVTVWQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYEPVNSRLSDIFRVVP-F--ISVEHI--PKGNNCLDAAKACNLDDICKKYRSAYITPCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TM---LANK-ECQAALEVIQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLASGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDS 119
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                                             Similarity 52.1% 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A S.,
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Similarity 48.1%; Pred. No. 0.00e+00;
222; Conservative 101; Mismatches 117; Indels
                                                                                                                                 1
18
431 AA;
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                                                                                                                                 17 F
431 G
47964 MW;
                                                              41.18;
52.18;
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50838 MW;
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H., OHNUMA N., TANABE M.,
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                                           Score
Pred.
81; M
                                                                                                                                 POTENTIAL.
GFR RECEPTOR ALPHA
, 7AE1F0B0 CRC32;
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                                             Mismatches
                                                              1392; DB 13;
No. 0.00e+00;
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                                                                                      Length
                                             Indels
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                                           11;
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Best Local :
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035118; PRELIMINARY;
035118; OTREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL D
GLIAL CELL LINE DERIVED N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. U.S.A. 0:00-0(1998).

EMBL; AB008833; D10244441; -.

EMBL; AF051766; G2961630; -.

MGD; MGI:1201403; GFRA3.

SEQUENCE 397 AA; 44307 MW; A80E0D24 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFRA3 OR GFRALPHA-3.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
"MOLECULAR CLONING And expression analysis of GFR
CDNA related to GDNER alpha and uTNR alpha.";
BIOCHEM. BIOPHYS. RES. COMMUN. 244:849-853(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98205811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GFRALPHA-3)
                                                                                                                                                                                                 337 KFLRDFTENPCLRNAIQAFGNGTNVNVSPKGPSF-QATQAPRVEKTPS-LPDDLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                      41 CTOARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS-VTPNCLDLRSFCRADPLCRSRLMDFQ
                                                                                                                                                    KPDSDLCLKFAMLCTLHDKCDRLRKAYGEACS-GI----RCQRHLCLAQLRSFFEKAAES
                                                                                                                                                                                                                                                                                                      CVRANELCAAESNCSSRYRTLRQCLAGRDRNTML--ANK--ECQAALEVLQESPLYDCRC
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                                                                                                                                                                                                                                                                                                                                                                                                   23.18;
l Similarity 38.28;
123; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05, CREATED)
05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                   Score 782; DB 11; L
Pred. No. 6.73e-172;
78; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                    211
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RESULT 11
1D 035325;
AC 035325;
AC 035325;
DT 01-JAN-1998 (TREMBLREL 05 DT 01-JAUG-1998 (TREMBLREL 05 DE GLIAL CELL LINE-DERIVED NE GN GFRA-3.

OS MUSCULUS (MOUSE).
CUKARYOTA; METAZOA; CHORDA OC SCIUROCNATHI; MURIDAE; MUFIDAE; MU
RESOLT
RE
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055243;
055243;
01-JUN-1998
01-JUN-1998
01-JUN-1998
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;
TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA
SUBMITTED (AUG-1997) TO EMBL, AF020305; G2429367; -
EMBL; AF02000841; -
EMBL; AF020305; -
EMBL; AF0205; -
EMBL; AF020
WIDENFALK SUBMITTED [2]
                                                                                                                                                                                                                                                                                                                                                                      GFRA3
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TREMBLREL 06, CREATED)
01-JUN-1998 (TREMBLREL 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL 06, LAST ANNOTATION UPDATE)
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY
                                          SEQUENCE FROM N.A. WIDENFALK J., TOMAC SUBMITTED (MAR-1998)
                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VI
SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFRA-3.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THCHPM-DILGTCATEQSR-CLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRGSGNLQ
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EECEKFLRDFTENPCLRNAIQA
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123; Conser
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                                               ) P.,
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY
                                 LINDQVIST E., HOFFER B
EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , IBANEZ C.F.;
EMBL/GENBANK/DDBJ DATA BANKS
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Matches 11
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Best Local Similarity 38.2%;
Matches 123; Conservative
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01-AUG-1998 (TREMBLREL. 07, LI
01-AUG-1998 (TREMBLREL. 07, LI
01-AUG-1998 (TREMBLREL. 07, LI
GDNF_FAMILY RECEPTOR ALPHA 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BALOH R.H.; GORODINSKY A., GOLDEN J.P., TANSEY POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
EMBL; AF051767; G2961632; -.
SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CH
CATARRHINI; HOMINIDAE;
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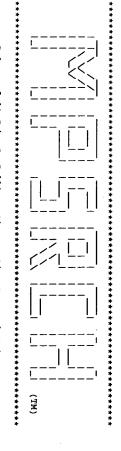
NAVELIHAN P., BAUDET C., MIKAELS O., SHEN L.,

PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).

EMBL; AF041842; G2921579; -.

EMBL; AF036163; G2674177; -.

SEQUENCE 397 AA; 44302 MW; F77607CF CRC32.
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                                                                                                          KPDSDLCLKFAMLCTLNDKCDRLRKAYGEACS---GP--HCQRHVCLRQLLTFFEKAAEP
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07, LAST SEQUENCE UPDATE)
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Pred. No. 6.73e-172;
78; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                            Score 705; DB 4; L
Pred. No. 5.00e-151;
88; Mismatches 94;
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Run on: MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm Thu Mar 11 13:52:56 1999; MasPar time 7286.84 Seconds 1372.471 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-866-354-35 (1-4232) from US08866354.seq 4232

1 CATGAAGAAACCTCAGTAAG......AAGGCTCCAATAAACGTGCG GTACTTCTTTGGAGTCATTC.....TTCCGAGGTTATTTGCACGC 4232

Scoring table: Gap TABLE default Gap 6

Nmatch STD Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_v1 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_v1 19:gb_in 20:gb_om 21:gb_ov 26:gb_pat 23:gb_ph 24:gb_ph 1 25:gb_ph 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_pr3 29:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_v1

Statistics: Mean 13.036; Variance 18.010; scale 0.724

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length DB	₽ 8	Ħ	Description Pred.
ב	2884	68.1	2906	28	HSU97145	S RET
2	1513	35.8		28	AF002700	sapiens
ω	1387	32.8		27	HSU93703	n qlial cell
4	1218	28.8		29	RNU97143	Rattus norvegicus RET
u	1147	27.1		29	AF005226	Rattus norvegicus glia
თ	1134	26.8	1392	29	AF002701	Mus musculus GDNF fami
7	830	19.6		29	AF079107	Mus musculus glial cel
œ	758	17.9		29	AF079108	Mus musculus glial cel
9	869	16.5		21	GGU90542	Gallus gallus neurturi
c 10	346	8.2		ω	G27011	human STS SHGC-31819.
11	223	5.3		29	RNU59486	Rattus norvegicus GDNF
12	223	5.3	3616	29	RNU97142	Rattus norvegicus RET
13	219	5 2		נ		

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56	54	56	56	54	55	55	54	55	56	61	58	58	58	58	66	66	66	71	88	102	129	131	131	161	161	166	164	183	212	212	217
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MMHC135G15	AC005878	MMMH461	AC004590	HS190A9	MMU67065	RNNTS1	95		HSA272ZE9	8	I66494	NU30	G41643	RNO231029	AC005872	HSGFRA1H02	\mathbf{r}	AB004258	I66494	GU9054	AC006095	HSGFRA1H05	8	HSU95847	HSU97144	AF015172	RN2072	S	F03842	208	AB000800
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ALIGNMENTS

C	7	gene					source	FEATURES	JOURNAL	TITLE			AUTHORS	REFERENCE	MEDLINE	JOURNAL			TITLE			AUTHORS	REFERENCE			ONGOVITOR	OPCANTCA	SOURCE	KEYWORDS	100000	DEFINITION	LOCUS	RESULT 1
/gene="RETL2"	/gene="RETL2"	12906	/tissue_type="liver"	/dev_stage="embryonic"	db xref="taxon: qsof=""	/organism="Homo saptens"	1 2906	Center, Cambridge, MA 02142, USA Location/Oualifiers	Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cambrida.	Direct Submission	Pepinsky, R.B. and Cate, R.L.	Walus, L. Robinson, S. Jaworski, G. Wei, H. Tizard, R. Whitty	Sanicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Ehren in Jan.	2 (bases 1 to 2906)	97322356	Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)	proteins	activation can be mediated by two different cell-surface access	Glial cell line-derived neurotrophic factor-dependent KET	Pepinsky, R.B. and Cate, R.L.	Walus, L., Robinson, S., Jaworski, G., Wei, H., Tizard, R., William	Sanicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Flant C.	1 (bases 1 to 2906)	HOMO,	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; mumi	SCHOOL SAFETERS	U0300000000000000000000000000000000000	human.	92202027	200007	HOMO Sapiens RET ligand 2 (RETL2) mRNA, complete cds.	HSU97145 2906 bp mRNA PRI 29-JH-	

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BASE COUNT
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1715	GCTGAAAGTTGGCCTTGTAGGCTGTGGGAACCGAGTCAGAAGATTTTTGAAAGCTACGCA ACAAGAACAGCCGCCTTGTAGGAAATGGAAACGAACACACAC	1689	5 S
:	TGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAGAATATTTTTGAAAGCTAKGKA	62	, D
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•	CATGTGCTTCACAGAGCTCACGACAAATATCATCCCAGGGAGTAACAAGG1&AAAAAGG1	1 6	ş Q
	GCATGTGCTTCACAGAGCTCACGACAAATATCCATCCCAGGGAGTAACAAGGTGATCAAAAA	1509	Db
<u>'</u> ;	TCACCACCTGCACGTCTGTCCAGGAGCAGGGGGCTGAAGGCCAACAACTCCAAAGAGTTAA	2782	Qy
1.1	CACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGGCCCAACACTCCAAAGAGTT	1449	.Db
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•	GGACGTGAACGTGTCCCCAAAAGGCCCCCTCGTTCCAGGCCACCCAGGCCCCTTca:::	1329	Дb
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-	CAGGGACTTCACCGAGAACCCATGCCTCCGGAACGCCATCCAGGCCTTTGGCAA::-:-	1269	DЪ
1_	TGTCCCCCTGGTGCAGCTGTCGTGGCAGCAGGAACATGGAGGAGGAGTGTGAGAACT	2542	Qy
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L CE	CATGATTGGGTTTGACATGACACCTAACTATGTGGACTCCAGCCCCACTGGCATCGTG	1149	뫄
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1148	CAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGGCGTGTCTGGGGCTCTTATGCT	1089	Дb
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2301	TGCTCTTCTGCTCCTGCCAAGACCAGGGGTGCGCTGAGGGCCCGCCAAACCATCCTGC	2242	Оу
968	GCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGCGCCGCCGGCAAACCATCCTG	909	ДD
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8	GTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGCCCAGCGAGTACACCTACCGC	4	Db .
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Query Match 35.8%; Best Local Similarity 99.7%; Matches 1522; Conservative

Score 1513; DB 28; Pred. No. 0.00e+00; 0; Mismatches 3

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1 (bases 1 to 1526)
Baloh,R.H., Tansey,M.G., Golden,J.P., Creedon,D.J.,
Heuckeroth,R.O., Keck,C.L., Zimonjic,D.B., Popescu,N.C.
Johnson,E.M. Jr. and Milbrandt,J.
TinR2, a novel receptor that mediates neurturin and GDN
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Baloh,R.H. and Milbrandt,J.D.
Direct Submission
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                                                                         /product="GDNE family receptor alpha 2"
/db_xref="pid:92145080"
/db_xref="pid:92145080"
/translation="MILANVFCLEFFLDETLRSLASPSSLQGPELHGWRPPVDCVKAN
ELCAAESNCSSSYRTLROCLAGRDRNTMLANKECQAALEVLQESPLYDCRCKRGMKKE
LQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNI
CLDAAKRACNLHDNCKKLRSSYISICNREISPTERCHRRKCHKALRGOFEDRVPSEYTYR
MLFCSCQDQACAERRROTLPSGSYEDKEKPNCLDLRGVGRTDHLCRSKLADFHAN':R
ASYQTVTSCPAANYQACIGSYAGNIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEE
CEKFLRDFTENPCLRNAIQAFGNGTDVNVSPKGPSCATQAPRVEKTPSLDDLSDST
                                        ALTVLSVLMLKQAL
                                                       SLGTSVITTCTSVQEQGLKANNSKELSMCFTELTTNIIPGSNKVIKPNSGPSRARPSA
                                                                                                                                                                                                                                                                                   /note="IGF-beta related neurotrophic factor
TRN receptor, GPI-anchored"
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Wartiovaara K., Suvanto P.,
Moshnyakov M., Airaksinen M
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Suvanto P., Wartiovaara K. and
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//translation="MILANAFCLEFELDETLRSLASDSSLQGPELHGWRPPVDCVKANV
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LQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGADPVVSAASG
CLDAAKACNLNDCKKLRSSYISICNEEISPTERCNRKCHKALRQFEDRVPSEYIVK
MLFCSCODQACAERRRGTILPSCSYEDKEK PNCLDLARGVCRTPHLCRSSRLADFHAAL
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CEKFLRDFTENPCLRNAIQAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGNGTDVNVATAFGN
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                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"GDNFR-beta"
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/note="forward PCR
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Query Match Best Local

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GACTTCACCGAGAACCCATGCCTCCGGAACGCCATCCAGGCCTTTGGCAACGGCACGAAC
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                                        GACTTCACCGAGAACCCATGCCTCCGGAACGCCATCCAGGCCTTTGGCAACGGCACGGAC
                                                                                        CCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGGAGGAGGAGTGTGAGAAGTTCCTCAGG
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U97143
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Submitted (11-APR-1997) Molecular
Center, Cambridge, MA 02142, USA
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1. .2787
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             AGACCACCTGTGCCGGTCCCGACTGGCAGATTTCCACGCCAACTGTCGAGGCCTACCG
                                            TTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCGCAGCCTGTGTCGTAC
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llarity 88.7%;
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JOURNAL Unpu REFERNCE 2 (AUTHORS Trug TITLE Dire JOURNAL Subn FEATURES DOK't FOUR SOURCE	OURCE ORGANISM EFERENCE AUTHORS TITLE	5 AFO TION Rat rec ION AFO 922	Oy 3026 AGAACAG	2966 GA	1500 GACCT	Db 1440 CTCAGG	Db 1380 GTGCT1 Qy 2846 GTGCT1	2786 CACCIG	2726 GACGO	1260 GACTC	Db 1200 TGTGAJ Qy 2666 CGTGAJ	2606 G	עץ בשיט כככבות	1080 T	Db 1020 GATTGO	426 GACGG	Db 960 GACAATC
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TTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACCATCCTGCCCAGT
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llarity 91.18;
Conservative
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/function="binds GDNF and allows GDNF binding to and stimulation of the c-Ret receptor tyrosine kinase"
/note="GPI-anchored receptor with sequence similarity GDNFR-alpha"
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MLFCSCQDQACAERRQTILPSCSYEDKEKPHCLDLRSLFHLCRSRLADFHANGR
ASYRTITSCPADNYQACIGSYAKMIGFDMTPNYVDSNPTGIVYSPWCNGRGSGNMEE
CEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDST
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/product="glial cell line-derived receptor-beta"
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/translation="MILANAFCLFFFLDETLRSLASPSSLQGSELHGWRPQVDCVRAN
/translation="MILANAFCLFFFLDETLRSLASPSSLQGSELHGWRPQVDCVRAN
ELCAAESNCSERYRTLRGCLAGRWKKE
LQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGTDPAVSTKSNH
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JOURNAL MEDLINE REFERENCE AUTHORS

2 (bases 1 to 1392)
Baloh,R.H. and Milbrandt,J.D.
Direct Submission

TITLE

through Ret

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(1997)

TrnR2, a novel receptor

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Baloh, R. H., Tansey, M.G., Golden, J. P., Creed Heuckeroth, R. O., Keck, C. L., Zimonjic, D. B., Johnson, E. M. Jr. and Milbrandt, J.
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/db_xref="piD:g2145082"
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/translation="MILANAFCLFFFLDETLRSLASPSSPOGSELHGWRPOVDCVRAN
/translation="MILANAFCLFFFLDETLRSLASPSSPOGSELHGWRPOVDCVRAN
ELCAAESNCSSRYRTLROCLAGRDRNVIMLANKECQAALEVLQESPLYDCRCKRGMKKE
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CEKFLKDFTENFCLRNAIQAFGNGTDVNNSPKGFTFSATQAFRVEKTFSLEDDLSDST
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REFERENCE AUTHORS TITLE

Rodentia; Sciurognathi; Muridae; Mu 1 (bases 1 to 1405) Wong, Y. W. and Too, H. P. Identification of mammalian GFRa-2 Neuroreport 9 (17) (1998) In press

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KEYWORDS SOURCE

ORGANISM

Eukaryota; Mus musculus house mouse.

Metazoa; Chordata; Vertebrata; Sciurognathi; Muridae; Murinae;

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Wong, Y. W. and Too,H.P.
Direct Submission
Submitted (20-JUL-1998) Biochemistry, National University of
Singapore, 10, Kent Ridge Crescent, Singapore 119260, Singapore
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/family receptor alpha 2b"
/fdb_xref="plD: g3941704"
/fub_xref="plD: g3941704"
/fub_xref="plD:
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329. .1405
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/db_xref="taxon:10090"
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Singapore, 10, Kent Ridge Crescent, Singapore 119260, Si. a.
Location/Qualifiers
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AF079108
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Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 1321)
Wong, Y.W. and Too, H.P.
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Mus musculus
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Neuroreport 9 (17) (1998) In press
2 (bases 1 to 1321)
Wong,Y.W. and Too,H.P.
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                            306
                            2
            LGSYAGMIGEDMIT NIVERPIGITOR DELICATION CRASPER TIRGE: "NI IQAFGNOTDVNMSPKGPTFSATOARPEEREEKFIKH-HING" LOAFGNOTDVNMSPKGPTFSATOARPUEKTPSLEDDLSGSTSLGTSVI ITV: SULKANNSKELSMCFTELTINISPGSKKVIKLYSGSCRARLSTALTALFLLMVI (1.7.1.3.1.4.1.2.1.2.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.1.3.1.3.1.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3
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                                                                                                                                     /codon_start=1
/product="glial cell line derived neurotrophic two-family receptor alpha 2c"
family receptor alpha 2c"
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TRSSYISICHREISPTERCHRRKCHKALRQFFDRVPSEYTYRMLPYSGUPGAV'N . . .
TILPSCSYEDKEKPNCLDLSSLCRTDHLCHSRLADFANCRASYRTTTSGUTALLT. . . .
                                                                                                                                                                                                                                                                                                                                                              /gene="Gfra2"
/note="GDNF family receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"Gfra2"
329. .1321
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/db_xref="taxon:10090"
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Direct Submission

Direct Submission

Submitted (24-FEB-1997) Biol. Med. Sciences, Univ. of Submitted (24-FEB-1997) Biol. Med. Sciences, Univ
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1 (bases 1 to 2933)
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/db_xref="pl0:92213805"
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DAAKACNLNDMCKRLASGZISTCSKESEISATEHCSRKKCHKALFQDFDNVPSETYYRLL-
DAAKACNLNDMCKRLASGZISTCSKESISATEHCSRKHCHKALFQDFDNVPSETYYRLL-
DAAKACNLNDMCKRLASGZISTCSKESISATEHCSRKHCHKALFQDFDNVPSETYYRLL-
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ACAGTATTAAAAAAAATAAACTTTACAATAATACATTTTCGCTCATCTGTTGGGGTA'IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Cho::::
Vertebrata; Eutheria; Primates; Catarrhini; Hominida:::
1 (bases 1 to 432)
Myers,R.M.
                                                                                                                                                                                                                                                                                                                                     Prepared with primer pairs provided by Sandoz, -- Washington University/Merck EST sequence.
Location/Qualifiers
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U59486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDNF-induced activation of the ret protein tyrosine mediated by GDNFR-alpha, a novel receptor for GDNF CELL 85 (7), 1113-1124 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fox, G.M., Jing, S.J., Yu, Y., Holst, P.L., Antonio, L., Hu, Z. and Louis, J.-C.
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Jing, S.J., Wen, D., Yu, Y., Holsi
Antonio, L., Hu, Z., Cupples, R.,
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Vertebrata; Eutheria;
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llarity 65.7%;
Conservative
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//db_xref-"piD:9139863"
//db_xref-"piD:9139863"
//translation-"MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
//translation-"MFLATLYFALPECRSAWEALKOKSLYNCRCKRGMKKEKNCLRI
KYRTLRQCVAGKETNFSLTSGLEAKDECRSAWEALKOKSLYNCRCKRGMKKEKNCLDAAKA
KYRTLRQCVAGKETNFSLTSGLEAKDECRSAWEALKOKSLYNCRCKRGMKLEKSCRL
KYRMYQSLQGNDLLEDSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKA
CNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALLQFFDKVPKHYSGMLFCSCRD
IACTERRQDTYUPVCSVEERERBRUCLSLQDSCKTNYIORSRLADFFTNQCPESRSVSN
CLKENYADCLLAYSGLIGTVMTPNYVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKD
MTCLKARIQAFGNGSDVTMWQDAPPVQTTTATTTAFRVKNKPLPAGSENEIPTHYL
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DROAN OALVENYGGNEIPTHYL
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/db_xref="taxon:10116"
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Eutheria; Rodentia; Sciurognathi; N
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                                                                                                                                                              Score 223; DB 29;
Pred. No. 4.10e-51;
0; Mismatches 297
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receptor alpha
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REFERENCE AUTHORS

Murinae; Rattus.

1 (bases 1 to 3616)
Sanichae, Hessinn,C.A., Worley,D.S.,
Sanichae, Hessinn,C.A., Worley,D.S.,
Walus,L., Robinson,S., Jaworski,G., Wei,
Pepinsky,R.B. and Cate,R.L.
Glial cell line-derived neurotrophic fac

factor-dependent

Carmillo, P., El, H., Tizard, R.,

Ehrenfels,C., Whitty,A.,

Muridae:

Rattus norvegicus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;

TITLE

SOURCE ORGANISM

Norway rat.

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KYRTLRQCVACKETNESITSGLEAKDECRSAMEAKOKSIYNCROKOKSKKCKR
YWSMYQSLQGUDLLEDSPYEFVNSKLESDIFRAVPFISDYFQQVEHISKGUNCLDAKA
CNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKYPAKHSYGMLFCSCRD
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CLKENYADCLLAYSGLIGTVMTPNYVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKD
NTCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKFLGPAGSENEIPTHVL
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/db_xref="PID:g2282022"
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/strain="Wistar"
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/dev_stage="embryonic day
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2 (bases 1 to 2549)
Dey, B.K., Wong, Y.W. and Too, H.
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/codon_start=1
/product="GDNF receptor alpha"
/db_xref="plD:g2624961"
/translation="MFLATLYFYLPLLDLLMSAEVSGGDRLDCVKASUJONA/
KYRTLROCVAGKETNFSLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKK:NN
YWSMYQSLQGNDLLEDSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNNN:
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/tissue_type="liver"
1. .2549
                                                                                                                                                                                                                       /strain-"C57"
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GGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCAAAAAGGCCCCCTCGTTCCAGGCCAC
                                    AGCCTTTGGCAATGGCTCGGATGTGACCATGTGGCAACCAGCCCCCCAGTCCAGACCAC
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                                                                       GGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCATGCCTCCGGAACGCCATCCA
                                                                                                                                               CCCCACTGGCATCGTGGTGCCCCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGGAGGA
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CLKENYADCLLAYSGLIGTVMTPNYIDSSSLSYAPWCDCSNSGNDLEDCKLKETAMFKD
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2 (bases 1 to 1415)
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Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1619)
Shefelbine, S.E., Khorana, S., Schultz, P.N., Huang, E.,
Hu, Z.J., Fox, G.M., Jing, S., Cote, G.J. and Gagel, R.F.
Mutational analysis of the GNF/RET-GDNFRA signaling
Direct Submission
          Hum. Genet. (1998) In press
2 (bases 1 to 1619)
Shefelbine, S.E., Khorana, S.,
Hu, Z.J., Fox, G.M., Jing, S.,
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                 CACTGCCACT 1208
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Search completed: Thu Mar 11 18:15:21 1999 Job time: 15745 secs.

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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 06:14:28 1999; MasPar time 3837.26 Seconds 1364.111 Million cell updates/sec

Tabular output not generated.

>US-08-866-354-39 (1-2215) from US08866354.seq 2215

Description:
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RESULT

Scoring table: TABLE default Gap 6

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Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb156

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_cor 8:em_cor 9:em_cor 10:em_pat 11:em_ph 12:em_pl 13:em_ror 14:em_un 15:em_v1

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16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi

Statistics: Mean 12.065; Variance 15.384; scale 0.784

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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_	1478	66.7	2787	29	RNU97143	Rattus norvegicus RET	0.00e+00
2	1355	61.2	1395	29	AF005226	norvegicus	0.00e+00
w	1252	56.5	1392	29	AF002701	CO.	0.00e+00
4	1159	52.3	2906	28	HSU97145	RET	0.00e+00
_G	1157	52.2	1526	28	AF002700	Homo sapiens GDNF fami	0.00e+00
თ	1116	50.4	1395	27	HSU93703	Human glial cell line-	0.00e+00
7	944	42.6	1405	29	AF079107	Mus musculus glial cel	6.39e-297
8	870	39.3	1321	29	AF079108	Mus musculus glial cel	5.13e-272
9	640	28.9	2933	21	GGU90542	Gallus gallus neurturi	8.32e-195
10	215	9.7	1415	29	AB000800	Mouse mRNA for GDNF re	4.77e-54
11	215	9.7	2549	29	AF014117	Mus musculus GDNF rece	4.77e-54
12	213	9.6	2138	29	RNU59486	Rattus norvegicus GDNF	2.12e-53
13	213	9.6	3616	29	RNU97142	Rattus norvegicus RET	2.12e-53

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ALIGNMENTS

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/gene="REIL2" /gene="REIL2"	/un_xiei- raxun:10110 /dev_stage="mbryonic" /tissue_type="brain/kidney" /1 2787	Center, Cambringe, ma 02142, USA 12787 12787 227	Pepinsky, R.B. and Cate, R.L. Direct Submission Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cumb of the Computer Computer of the Computer of th	Dases 1 to 2787) 2 (bases 1 to 2787) Sanicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Ehronton, C.A., Walus, L., Robinson, S., Jaworski, G., Wei, H., Tizard, R., White A.	proteins Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997) 07377356	Pepinsky R.B. and Cate R.L. Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface activation	Murinae; Rattus. 1 (bases 1 to 2787) Sanicola,M., Hession,C.A., Worley,D.S., Carmillo,P., Ehrenation, C. Murinae; Rattus.	Norway rat. Norway rat. Rattus norvegicus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridue:	RNU97143 2787 bp mRNA ROD 29-JUL-1997 Rattus norvegicus RET 11gand 2 (RETL2) mRNA, complete cds. U97143 g2282023

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Rattus norvegicus glial cell line-derived neurotrophic factor
receptor-beta (GDNFR-beta) mRNA, complete cds.
AF005226
g2232251
Direct Submission
Submitted (23-MAY-1997) Neuroscience, Karo
Doktorsringen 12A, Stockholm 17177, Sweden
Location/Qualifiers
                                                                                          1 (bases 1 to 1395)
Trupp,M., Raynoschek,C. and Ibanez,C.F.
Multiple GPI-anchored receptors control GDNF-dependent and independent activation fo the c-Ret receptor tyrosine kings uppublished
                                                                                                                                                                                      Rattus norvegicus
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Trupp, M., Raynoschek, C. and Ibanez, C.
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CGAGTATACCTACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCG
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                                                                                                                                                                                                                                                 CTGCAAGAAGCTTCGCTCCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGA 578
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                                                                                                                                         ACGCTGCAACCGCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAG
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                                                                                                          ACGCTGCAACCGCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAG 1309
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llarity 99.9%;
Conservative
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/translation="MILANAFCLFFFLDETLRSLASPSSLQGSELHGWRPQVDCVRAN
/translation="MILANAFCLFFFLDETLRSLASPASSLQGSELHGWRPQVDCVRAN
/translation="MILANAFCLFFFLDETLRSLASPASSLAGSELHGWRPQVDCVRAN
/translation="MILANAFCLFFFL"
/translation="MI
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receptor-beta"
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1. .1395
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Pred. No. 0.00e+00;
0; Mismatches 1;
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TITLE JOURNAL MEDLINE FERENCE AUTHORS TITLE JOURNAL	YWORDS URCE ORGANIS	SULT CUS FINITION	20	1359	129	1910	1239	1179 1850		111	1059	1670	161	939	1550	87	1490	. 1	7	1370	699
Heuckeroth,R.O., Keck,C.L., Zimonjic,D.B., Popescu,N.C., Johnson,E.M. Jr. and Milbrandt,J. TINR2, a novel receptor that mediates neurturin and GDNF signaling through Ret Neuron 18 (5), 793-802 (1997) 97325791 2 (bases 1 to 1392) Baloh,R.H. and Milbrandt,J.D. Direct Submission Submitted (06-MAY-1997) Pathology, Washington University, 660 South Euclid Ave, Box 8118, St. Louis, MO 63110, USA	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Mammal Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1392)	3 AF002701 1392 bp mRNA ROD 02-MAR-1998 N Mus musculus GDNF family receptor alpha 2 (GFRalpha2) mRNA, COMPLETE Cds. AF002701	0	TAAAAAAGITAATCAAACTTAACTCAGGCTCCAGCAGAGCCAGAGTGTCGGCTGCCTTGAC 2::::	TAAAAAGGTGATCAAACTTAACTCAGGCTCCAGCAGAGGCCAGACTGTCGGCTGCCTTGAC ' ',	CAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAARRINE	CAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGGAG 🙁 🖟	CCTGGGGACCAGTGTCATCACCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCAA 1.24,	CCAGGCCCTCGGGTGGAGAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCAC(:AC) 15.7	CCAGGCCCCTCGGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGUAG: A	GGCCTTTGGTAATGGCACAGATGTGAACATGTCTCCCAAAGGCCCCTCACTCCAAGCOACOACOACOACOACOACOACOACOACOACOACOACOAC		CCCCACGGGCATCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAANA · ·	CCCCACGGGCATCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGCAAA, ^ ;-	TCTGGGCTCCTATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAA	CTGGGCTCCTATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAA	CAACTGTCGAGCCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATG 878	:	CCTGCGCAGCCTGTGTCGTACAGACCAGCCTGTGCCGGTCCCGACTGGCAGATTTCCACGC 818	CCGGCAAACCATCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGA 1429	CCGGCAAACCATCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGA 758

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                                                                                                                                                                 GGTCAGTGCCAAGAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAACGACAA 518
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                                                 ACGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGTGTGCCCAG
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larity 96.3%;
Conservative
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//db_xref="pID:g2145082"
//db_xref="pID:g2145082"
//translation="MILANAFCLEFFLDETLRSLASPSSPOGSELHGWRPQVDCVRAN
/translation="MILANAFCLEFFLDETLRSLASPSSPOGSELHGWRPQVDCVRAN
/translation="MILANAFCLEFFLDETLRSLASPSSPOGSELHGWRPQVDCVRAN
/translation="MILANAFCLEFFLDETLRSLASPSSPOGSELHGWRKKE
LCAABSNCSSRYRTLRQCLAGBRORNTMLANKECQAALEVLQESPLYDCRCKRGMKKE
LOCLOIYWSIHLGLTEGGEFYEASPYEPVTSRLSDIFRLASIFSGTGADVVSAKSNH
CLDAAKACNLNDNCKKLASSYISCUREISPTERNRCHKALRQFFDRVPSEYTYR
MLFGSCODQACAERRRQTILPGSCYEDKERPNCLDLRSLCRTDHLRCGRSRLADFHANCR
ASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEE
CEKFLKDFTENPCLRNAIQAFGNGTDVNNSPKGPTFSATQAPRVEKTPSLPDDLSDST
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1. .1392
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/function="mediates neurturin and GDNF signaling through
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/db_xref="taxon:10090"
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Pred. No. 0.00e+00;
0; Mismatches 50;
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                                                Sanicola, M., Hession, C.A., Worley, D.S. Walus, L., Robinson, S., Jaworski, G., W Pepinsky, R.B. and Cate, R.L. Glial cell line-derived neurotrophic activation can be mediated by two dif
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U97145
                         Proc. Natl. Acad. Sci.
                                     proteins
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Vertebrata;
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Walus,L., Robinson,S., Jaworski,G., We
Pepinsky,R.B. and Cate,R.L.
Direct Submission
Submitted (11-APR-1997) Molecular Gene
Center, Cambridge, MA 02142, USA
Location/Qualifiers
                                                                                              AGAGCCCGCTGTACGACTGCCGCTGCAAGCGGGGCATGAAGAAGAAGGAGCTGCAGTGTCTGC
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GCGAGATCTCGCCCACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGT
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SLGTSVITTCTSVQEQGLKANNSKELSNCFTELTTNIIPGSNKVIKPNSGPSRARPSA
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/note="PI-linked cell-surface accessory protein"
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/dev_stage="embryonic"
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SOURCE ORGANISM

human. Homo sapiens

DEFINITION
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Homo sapiens of complete cds. AF002700 g2145079

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                                             TGGGAACCGAGTCAGAATATTTTTGAAAGCTACGCAGACAAGAACAGCCGCCTGACCAAA
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Direct Submission
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TRN receptor, GPI-anchored"
/codon_start=1
/product="GDNF family receptor alpha 2"
/db_xref="PID:g2145080"
//translation="MILANVFCLFFFLDETLRSLASPSSLOGPELHGWRPPVDCVRAN
LTCAALSNCSSRYRTLRQCLAGADRNTMLANKECQAALEVLQESPLYDCRCKRGKKE
LQCLOLYWS-HIGLTEGEEFYEASPYEDVTSRLSDIFRLASIFSGTGADPVVSAKSNH
CLDAAKACNLNDNCKKLRSSYISICNREISPTERCMRKCHKALKOFEDRVPSEYTYR
MLFCSGQDQACAERRROTILPSCSYEDKEKPNCLDLRGVCRTDHLCRSRLADFHANCR
ASYOTVTSCBADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEE
CEKFLRDFTENPCLRNAIQAFGNGTDVNVSPKGPSFQATQAPRVEKTPSLFDDLSDST
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/function="mediates neurturin and GDNF signaling through
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CLDAAKACNLNDNCKKLRSSYISICNEEISPTEERUNRRKCHKALRQFEPRVPSEYTYR
MLFCSCQDQACAERRQTILPSCSYEDKEKPNCLDLRGVCRTDHLCRSRLADFHANCR
ASYQTVTSCPADNYQACLGSYAGNIGFDMTPNVDSSPTGIVVSPWCSGCRGGNMEEE
CEKFLRDFTENPCLRNAIQAFGNGTDVNVSPKGPSFQATQAPRVEKTPSLPDDLSDST
SLGTSYITTCTSVQEQGLKANNSKELSMCFTELTTNIIPGSNKVIKPNSGPSRARPSA
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/product="glial cell line-derived neurotrophic factor receptor beta"
/db_xref="plD:g2228737"
/db_xref="milanafclefflderinglashSpSSLQGPELHGWRPPVDCVRAN
/translation="MilanafclefflderinglashSpSSLQGPELHGWRPPVDCVRAN
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Wong, Y.W. and Too, H.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification of mammalian GFRa-2 splice isoforms Neuroreport 9 (17) (1998) In press 2 (bases 1 to 1405) Wong, Y. W. and Too, H. P. Direct Submission
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//note="GDNF family receptor alpha 2b"
//note="GDNF family receptor alpha 2b"
//codon_start=1
//codon_start=1
//product="gilal cell line derived neurotrophic factor
family receptor alpha 2b"
//db_xref="piD:g3941704"
//translation="MILANAFCLFFELGEEFYEASPYEPUTSRLSDIFRLASIFSGTG
ADPVVSAESNHGLDAKACNLANNCKKLRSSYISICNREISPTERCNRRKCHKALRQF
FDRVPSEYTYRMLFCSCODQACAERRQTILPSCSYEDKEKPNCLDLRSLCRTDHLCR
SRLADEHANCRASYRTITSCPADNYQACLGSYAGNIGEDMETWIDSNEPGIVVSSWC
NCRGSGNMEEECEKFLKDFTERDCLRNLOAFGNGTDVUNMSPKGPTEATQAFRVEKT
PSLPDDLSDSTSLGTSVITTCTSIQEQGLKANNSKELSNGFTELTTNISPGSKKVIKL
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REFERENCE AUTHORS

Rodentia; Sciurognathi; Muridae; Mu 1 (Dases 1 to 1321) Wong,Y.W. and Too,H.P. Identification of mammalian GFRa-2 Neuroreport 9 (17) (1998) In press

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Eukaryota; Rođentia; S

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 AAAACCCATGCCTCCGGAATGCCATTCAAGCCTTTGGCAATGGCACAGATGTGAACATGT
                                                   ATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGAGAAGTTCCTCAAGGACTTCACAG
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Wong, Y.W. and Too,H.P.
Direct Submission
Submitted (20-JUL-1998) Biochemistry, National Univerrsity of
Singapore, 10, Kent Ridge Crescent, Singapore 119260, Singapore
Location/Qualifiers
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/db_xref="plic;g3941706"
/db_xref="plic;g3941706"
/translation="MilanaFCLFFFLGTGADPVVSAESNHCLDAAKACNLNDNCKKL RSSYISICNREISPTERCNRRKCHKALLQFFDRVPSEYTYRMLFCCSCQDQACAERRRQ TILPSCSYEDKEKPNCLDLRSLCRTDHLCRSRLADFHANCRASYRTITSCPADNYQAC LGSYACMIGFDMTPNYVDSNFTGIVVSDENCKRGSGINHEEECEKFLKDFTENPCLNA IQAFGNGTDVNNSPKGIPTSATQAPRVEKTPSLPDDLSDTSLGTSVITTCTSIQEQG LKANNSKELSMCFTELTTNISPGSKKVIKLYSGSCRARLSTALTALPLLMVTLA"

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/note="GDNF family receptor alpha
/codon_start=1
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/db_xref="taxon:10090"
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Pred. No. 5.13e-272;
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Query Match

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Gallus ga
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Submitted (24-FEB-1997) Biol. Med. So
Bute Medical Buildings, St. Andrews,
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Buchman, V.L.
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                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/db_xref="taxon:9031"
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AGCCTTCGGCAATGGCACCGATGTCAACCTCTCCCCCAAGAAACCCCTCACCTCCCATCAC
                                                    GGAGTGTGAGAAGTTCCTGCGGGACTTCACTGAGAACCCCTGTCTCCGAAATGCTATCCA 1089
                                                                                          CCCCACGGCATCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGA
                                                                                                                    CACCACCAGCATCACTATCTCGCCCTGGTGCTCCTGCAAAGGCAGCGGCAACTTGGAGGA 1029
                                                                                                                                               TCTGGGCTCCTATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCCAA
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961; Conservative
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Mouse mRNA
AB000800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-JAN-1997) to the DDBJ/EMBL/GenBank databases. Kazuhiko Watabe, Tokyo Metropolitan Institute for Neuroscience Neuropathology; Musashidal 2-6, Fuchu, Tokyo 183, Japan (E-mail:kazwtb@tmin.ac.jp, Tel:0423-25-3881, Fax:0423-21-8678) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulation of GDNF receptor Unpublished (1997)
2 (bases 1 to 1415)
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GDNF receptor alpha.
Mus musculus Dorsal root ganglion
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Direct Submission
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Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi;
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larity 65.4%;
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/db_xref="plD:dl01934"
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/translation="MFLATLYFVLPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSGST
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VMACTERRAQTIVEVCSYBERERCLNLQDSCKTNYICRSRLADFFTNGQPESKSVSN
CLKENYADCLLAYSGLLGTVMFNYIDSSSLSVAPMCDCSNSGNDLEDCLKFLMFN-N
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/cell_line="IMS32"
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/db_xref="taxon:10090"
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Pred. No. 4.77e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCTAACTACATAGACTCCAG 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACTGTCGAGCCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGAGCCTG-CAG--GGAAATGACCTACTGGAAGATTCCCCATACGAGCCGGTTAACAG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCTTTGGTAATGGCACAGATGTGAACATGTCTCCCAAAGGCCCCTCACTCC
                                                                                                                                                                                                                                                                                                                                                AGATTGCCTGAAGTTTCTGAATTTTTTAAGGACAATACGTGTCTCAAAAATGCAATTCA 1029
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                                                                                                                                                      Mus musculus
AF014117
g2624960
             Rodentia; Sciurognathi; Muridae; N
1 (bases 1 to 2549)
Dey,B.K., Wong,Y.W. and Too,H.P.
Cloning of a novel murine isoform
neurotrophic factor receptor
                                                                                      Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata;
Neuroreport 9
                                                                                                                            house mouse
                                                                                                                                                                                                     AF014117
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GDNF
 (1) (1998) In
                                                                                                                                                                                     bp mRNA ROD 20. receptor alpha (GDNFR-alpha) mRNA,
press
                                                                            Murinae;
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                                                                                       CAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACGTCGCCTGCACCGAGAGGCG
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CCGGCAAACCATCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGA
                           GCGACAGACTATCGTCCCTGTGTGCTCCTATGAAGAACGAGAGAGGCCCAACTGCCTGAA 1647
                                                                                                                                  AGTCTGCAACCGCCGCAAAGTGCCACAAAGCCCTCAGGCAGTTCTTCGACAAAGTTCCAGC
                                                                                                                                                                                                                                    GGTCAGTACCAAAAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAATGACAA
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                                                           CGAGTATACCTACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCG
                                                                                                                                                                          CTGCAAGAAGCTTCGCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCCACCGA
                                                                                                                  ACGCTGCAACCGCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2549)
Dey,B.K., Wong,Y.W. and Too,H.P.
Direct Submission
Submitted (15-UUL-1997) Blochemistry,
Singapore 119360, Singapore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 9.7%;
Similarity 65.4%;
584; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="GDNFR-alpha"
914. .2320
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/codon_start=1
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Pred. No. 4.77e-54;
0; Mismatches 297;
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    ch 9.6%;
l Similarity 65.3%;
583; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNF-induced activation of the ret protein tyrosine kinase mediated by GDNFR-alpha, a novel receptor for GDNF Cell 85 (7), 1113-1124 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAY-1996) Immunology, Thousand Oaks, CA 91320-1789, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 2138)
Jing,S.J., Wen,D., Yu,Y., Holst,P.L., Luo,Y., Fang,M., Tamir,R.,
Antonio,L., Hu,Z., Cupples,R., Louis,J.-C., Hu,S., Altrock,B. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norway rat.
Rattus norvegicus
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U59486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fox, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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                                                                                                     494
                                                                                               /product="gDNF receptor alpha"
//db_xref="pID:g1399863"
//translation="mFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
/translation="mFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
KYRTLRQCVAGKETNFSLTSGLEAKDECKSAMEALKQKSLYNCRCKRGMKKEKNCLRI
YWSMYQSLQGNDLLEDSPYEPVNSKLSDJFRAVPFISDYGQVEBISKGNNCLDAAKA
CNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHALRQFFDKVPAKHSYGMLFCSCRD
IACTERRRQTIVPVCSYEERERRNCLSLQDSCKTNYICKSRLADFFTNCQPESRSYSN
CLKENYADCLLAYSGLIGTVMTPNYVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKD
NTCLKNAIQAFGNGSDYMMQPAPPVQTTTATTTTAFRVKNKPLGPAGSENEIPTHYL
PPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPV
LMLTALAALLSVSLAETS"
94 a 593 c 584 g 467 t
                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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Score 213; DB 29;
Pred. No. 2.12e-53;
0; Mismatches 298;
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MALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activa can be mediated by two different cell-surface accessory proteins. PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).

EMBL: U97145; G2282028: -

SEQUENCE 464 AA; 51543 MW; 288A8BDB CRC32;
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
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Best Local S
Matches 42
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O15316;
O1-JAN-1998 (TREMBLREL O5, CREATED)
O1-JAN-1998 (TREMBLREL O5, LAST SEQUEN
O1-AGG-1998 (TREMBLREL O7, LAST ANNOTI
GLIAL CELL LINE-DERIVED NEUROTROPHIC FI
GDNFR-BETA.
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TISSUE-FETAL BRAIN;
TISSUE-FETAL BRAIN;
WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL
MOSHNYAKOV M., AIRAKSINEN M.S., PALOTIE A., SARIOLA H., S
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U93703; G2228737; -
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
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il Similarity 94.0%;
426; Conservative
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LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
"GOTROPHIC FACTOR RECEPTOR BETA.
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Pred. No. 0.00e+00;
17; Mismatches 10
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. un on: Mon Mar 8 14:31:36 1999; MasPar time 36.56 Seconds 694.068 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-866-354-40 (1-460) from US08866354.pep 3343 1 MLVFPSHYPDETLRSLASPS......RARLSAALTALPLLMLTLAL 460

Scoring table: PAM 150 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl8
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.029; Variance 73.182; scale 0.643

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
3268 3131 3120 1541 1539 1523 1523 1520 1577 777 777 777 777 777 107 107 107	Score
97.8 93.3 93.3 221.2 221.2 3.1 3.1 3.1 3.1 3.1 3.1 3.1 3.1 3.1 3.1	Query Match
464 464 468 463 463 463 463 397 397 1016 11016 1703 1703 1703 1703 1703 1703 1703 1703	Length
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035977 015328 015326 035246 035748 035748 035752 035252 035252 015507 0935118 035325 0	Ħ
GLIAL CELL LINE-DERIVE RET LIGAND 2. GLIAL CELL LINE-DERIVE GDNF RECEPTOR ALPHA. GDNFF RECEPTOR BETA. GDNFF RECEPTOR BETA. RET LIGAND 1. GFR RECEPTOR ALPHA 4 P GLIAL CELL LINE-DERIVE	Description
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0	Ħ.	LIN-1 (FRAGMENT	6.2	HYPOXIA-INDUCIBLE HIG-	PROTEIN S PRECURSOR.	0	FISSION YEAST (FRAGMEN		NONSTRUCTURAL PROTEIN	ENVELOPE GLYCOPROTEIN	F18C12.1.	PROTEI	HEPATITIS A VIRUS CELL	IN (FRAGM	HYPOTHETICAL 45.5 KD P	HRPJ.	DCIAE PROTEIN.	F35E8.7.	TRANSCRIPTIONAL REGULA	19.7 KDA PROTEIN.	MYTONIC DYSTROPHY KINA	GENA	BY C.	CODED FOR BY C. ELEGAN
1.18e+00		•	2.32e+00	1.66e+00		•	•	1.66e+00	1.66e+00		.94e	5.94e-01	. 95e	4.19e-01	. 95e	.94e	.19e	.94e	5.94e-01		.07e-	.01e	2.34e-02	2.34e-02

ALIGNMENTS

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Best Local S
Matches 20
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O35252;
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
STRAIN-C57;
STRAIN-C57;
DEY B.K., WONG Y.W., TOO H.D.;
DEY B.K., WONG Y.W., TOO H.D.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF015172; G2624963; -.
STOTENCE 463 AA; 51134 MW; 910EF17F CRC32;
                                                                                                                                                                                        STRAIN=C57;
DEY B.K., WONG Y.W., TOC
NEUROREPORT 9:0-0(0001).
                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VI
SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                         GDNF RECEPTOR BETA. GDNFR-BETA.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRVKNKPLGPAGSENEIPTHYLPPCANLQAQKLKSNVSGNTHLCISN 417 : : | : : | | | | | : : | : :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGTVMTPNYIDSS-S-LSVA::|||||||||||||||:|::||:||
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AF038418; G2921545;
AF038418; G2921545;
AF042080; G2801557;
AF038421; G2921532;
AF058999; G3068783;
AF058991; G3068783;
AF058992; G3068783;
AF058993; G3068783;
AF058994; G3068783;
AF058994; G3068783;
AF058995; G3068783;
AF058997; G3068783;
AF058996; G3068783;
AF058997; G3068783;
AF058998; G3068783;
AF058998; G3068783;
AF058998; G3068783;
AF058998; G3068783;
AF058998; G3068783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRS
| ::|: | ::||::| | ::||::|||||::|
LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
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LASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKC
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l Similarity 50.6%;
206; Conservative
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JOINED
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 0.00e+00;
91; Mismatches 97;
                                                                                                                                                                                                                                                                                                                          VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                    BANKS.
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                                                                                                                                                                                                                                                                                                                       EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                       RODENTIA
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RESULT
ACCORDANCE
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Best Local S
Matches 21
                                                                                                                                                                                                                 FISSUE-KIDNE; 9732336.

MEDLINE; 9732336.

SANTOOLA M., BESSION C.A., WORLEY D.S., CARMILLO F., SANTOOLA M., BESSION C.A., WORLEY D.S., WEI H., TIZARD R., WHITTY A., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";

"ATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
                                   SEQUENCE FROM N.A.
TISSUE-SUBSTANTIA NIGRA;
HISHIKI T., KONDOH K., ICH;
SAKIYAMA S., TAKAHASHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015507
015507;
015507;
01-JAN-1998
01-JAN-1998
01-NOV-1998
    SUBMITTED
                                                                                                                                    SANICOLA M., HESSION C.A.,
WALUS L., ROBINSON S., JAW
PEPINSKY R.B., CATE R.L.;
SUBMITTED (APR-1997) TO EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RETLI.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HITTKSMAAPPSCGLSSLPVMVFTALA 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVI
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  (OCT-1997)
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B (TREMBLREL.
B (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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larity 48.1%;
Conservative
  ö
                                                                                                                                                                         .A., WORLEY D
JAWORSKI G.,
                                   ICHIMIYA S., N.
EMBL/GENBANK/DDBJ
                                                                                                                                    EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805,
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Pred. No. 0.00e+00;
102; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                            D
                                     NIMURA Y.
                                                                                                                                                                         WEI
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                                                                                                                                                                       CARMILLO P.
H., TIZARD
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                                                                                                                                    DATA
DATA
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BANKS
                                                          SEKI N.,
                                                                                                                                    BANKS
                                     FUJIMURA
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                                                                                                                                                                         EHRENFELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
                                                     OZAKI
                                     S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMATES;
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RESULT ACCOUNTS RESULT OF THE PROPERTY OF THE 
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                                                                                                                                                            ULT 5
035748; PRELIMINARY;
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
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4
O35246;
O35246;
O1-JAN-1998 (TREMBLRE
O1-JAN-1998 (TREMBLRE
O1-JAN-1998 (TREMBLRE
O1-JAN-1998 (TREMBLRE
GDNF RECEPTOR ALPHA.
GDNFR-ALPHA.
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STRAIN-C57; TISSUE-LLYLA,
DEY B.K., WONG Y.W., TOO H.P.;
DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JUL-1997) TO EMBL; AFDCE6A1 CRC32;
TOTTONICE 468 AA; 51751 MW; AFDCE6A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNER-ALPED,
MUS MUSCULUS (MOUSE),
EUKARYOTA; METAZOA; CHORDATA; VI
GDNFR-ALPHA/TRNR1-DELTA PROTEIN. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VE SCIUROGNATHI; MURIDAE; MURINAE; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57; TISSUE=LIVER;
DEY B.K., WONG Y.W., TOO H.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHLCRSRLADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKALRQFFDKVPAKHSYGMLFCSCRDVACTERRRQTIVPVCSYEERERPNCLNLQDSCKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HITTKSMAAPPSCGLSSLPVMVFTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRIKNKPLGPAGSENEIPTHYLPPCANLQAQKLKSNYSGSTHLCLSDNDYGKDGLAGASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRV-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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(TREMBLREL.)
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.1%;
larity 47.9%;
Conservative
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                                     CHORDATA; VERTEBRATA; MAMMALIA; AE; MURINAE; RATTUS.
                                                                                                                                                         05, CREATED)
05, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDAT
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Pred. No. 0.00e+00;
103; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , CREATED)
, LAST SEQUENCE UPI
, LAST ANNOTATION (
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E; MUS.
                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                      UPDATE)
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                                                                       EUTHERIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                       RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RODENTIA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-HANNOVER;
ZHONG J., ANNIES M., HEUMANN R.;
SUBMITTED (CCT-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;
  434
                                                                                    317
                                                                                                        306
                                                                                                                               257
                                                                                                                                                                         197
                                                                                                                                                                                             188
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                                                                                                                            LMSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRS
           HITTKSMAAPPSCSLSSLPVLMLTALA 452
                                           -KIPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTINISPG%KKVI (
                                                                                                                                                                                                                                                                       AMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR 134
   KLNSGSSRARLSAALTALPLLMLT-LA
                                                        FRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASS
                                                                                   PWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRV-E
                                                                                               PWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTA
                                                                                                                                                                                                                                                                                                      LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
                                                                                                                                                                                                                                                           ALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSD1FF
                                                                                                                                                                                                                                                                                                                                                219;
                                                                                                                                                                                                                                                                                                                                               h 46.0%;
Similarity 49.0%;
219; Conservative
                                                                                                                                                                                                                                                                                                                                               Score 1539; DB 11;
Pred. No. 0.00e+00;
97; Mismatches 112
                                                                                                                                                                                                                                                                                                                                                Mismatches 112;
   459
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                Indels 19;
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TRESULT OF TARREST OF 
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O43912;
O43912;
O1-JUN-1998 (TREMBLREL. 06, CF)
O1-JUN-1998 (TREMBLREL. 07, L)
O1-AUG-1998 (TREMBLREL. 07, L)
   EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFRA1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                 ANGRIST M., JING S., E FOX G.M., CHAKRAVARTI GENOMICS 0:0-0(1998).
                                                                                                                                                                                                                                                  FOX'G.M., JING S., COTE (
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-MEDULLARY THYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
4. GENET. 0:0-0(1998).

II. AFO38420; G2921545; JL: AFO38411; G2921545; J

II. AFO38412; G2921545; J

III. AFO38413; G2921545; J

III. AFO38414; G2921545; J

III. AFO38415; G2921545; J

III. AFO38416; G2921545; J
                                                                                                                                                                                                                                                  HYROID CARCINOMA TUMOR;
HORANA S., SCHULTZ P.N.,
COTE G.J., GAGEL R.F.;
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I A.;
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      JOINED
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENTLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NALLASAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAMMALIA;
                                                                                                                                                                                                                                                                                         HUANG
                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                         THOBE
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PRT;

465

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(MT)

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:05:53 1999; MasPar time 16.83 Seconds 739.942 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-866-354-36 (1-464) from US08866354.pep 3386 1 MILANVFCLFFFLDDTLRSL.....RARPSAALTVLSVLMLKLAL 464

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 1:swissprot

Statistics:

Mean 48.016; Variance 67.910; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					00.000		
Result	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
ב	3372	99.6	464	إد	NRTR_HUMAN	NEURTURIN RECEPTOR ALP	0.00e+00
N	3203	94.6	463	1	NRTR_MOUSE	RECEPTOR	0.00e+00
ω	2686	79.3	465	r	NRTR_CHICK	NEURTURIN RECEPTOR ALP	0.00e+00
4	1554	45.9	468	_	GDNR_RAT	GDNF RECEPTOR ALPHA PR	0.00e+00
Ç	1527	45.1	468	<u>, , , , , , , , , , , , , , , , , , , </u>	GDNR_MOUSE	RECEPTOR	0.00e+00
σ	1521	44.9	464	Ь	GDNR_HUMAN	ALPHA	0.00e+00
7	1501	44.3	469	1	GDNR_CHICK	GDNF RECEPTOR ALPHA PR	0.00e+00
80	100	3.O	452	_	EFTU_HUMAN	ELONGATION FACTOR TU,	
9	103		1712	1	TGFB_RAT	LATENT TRANSFORMING GR	9.87e-03
10	97		354	۲	NOVLMOUSE	NOV PROTEIN HOMOLOG PR	9.98e-02
11	95		113	L	RL19_MYCTU	50S RIBOSOMAL PROTEIN	2.10e-01
12	95	2.8	408	L	B3AR_HUMAN	BETA-3 ADRENERGIC RECE	.10e-
13	91		342	۰	CYS2_HAECO	CATHEPSIN B-LIKE CYSTE	.96e-
14	91	•	342	۰	CYS1_HAECO	CATHEPSIN B-LIKE CYSTE	
15	91	2.7	352	٢	ASP2_BLAGE	ASPARTIC PROTEASE BLA	
16	91	2.7	428	٢	MOD5_YEAST	TRNA ISOPENTENYLTRANSF	8.96e-01
17	16	2.7	437	ш	NO55_HUMAN	NUCLEOLAR AUTOANTIGEN	8.96e-01
18	93	2.7	452	۲	EFTU_BOVIN	ELONGATION FACTOR TU,	4.37e-01
19	90	2.7	513	_	HDAC_MAIZE	PROBABLE HISTONE DEACE	
20	91	2.7	521	_	GAG_SIVAG	GAG POLYPROTEIN (CORE	8.96e-01
21	93	2.7	799	μ	TRKA_RAT	HIGH AFFINITY NERVE GR	
22	91	2.7	879	۲	LDLR_RAT	LOW-DENSITY LIPOPROTEI	8.96e-01
23	92	2.7	1603	H	PSC_DROME	POSTERIOR SEX COMBS PR	6.27e-01

ALIGNMENTS

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B 0	SQ	14	Ŧ	FT	Ŧ	FT	Ŧ	ΗŢ	3	3	X	X.	DR	DR	88	3	S	ဂ	S	8	88	음	ဂ	2	₹	R.A	ŖΑ	RX	RP	RN	റ്റ	გ	ပ္တ	S	H	B	Ħ	ဌ	Ŋ	Ŋ,	č	ij	RESULT
Query Match Best Local	SEQU	LIPID	CARI	CARI	CARI		PROPER		CHAIN	SIGNAL	ALTI	REC	MIM.	EMBL:	:		<u>:</u>		:				<u>:</u>	NEU	THOL	HEUC	BAL(MEDI	SEQ	Ξ	EUTI	EUK	MOH	GFRA2	9	BET	NEC	15-	21-1	01-	000	NRT	H
Match ocal	VARSPLIC SEQUENCE	Ð	CARBOHYD	CARBOHYD	CARBOHYD		PEP		Z	Ā	ALTERNATIVE	PTOR	~ .	ΑF	IMIS	1105	ALTE	IMIS	SUBC	RECE	NO.	AUTO	FUNC	õ 1	SON	KERO	¥ R	MEDLINE;	SEQUENCE		EUTHERIA;	ARYOT	HOMO SAPIENS	S OR	(GDNFR-BETA)	REL	TURI	15-JUL-1998	ŃУ-1	1-70	000451:	HUM	r
Simil	4										IVE 9	<u>မ</u>	601956:	AF002700:	SIMILARITY:	SPLICING	ALTERNATIVE	SIMILARITY)	SUBCELLULAR	RECEPTOR.	MEDIATE	PHOSI	TION	8:79		THR	Ħ.,	973			PR	A; Mi	IENS	CDNI	ETA	ATED	Z REC					A ·	
similarity	14 64 AA;	444	413	357	52		445		22	ب ـم	SPLICING	COPR						•		i	E GDNF	HORY	REC	3-802	JOHNSON E.M. JR.,	0	BALOH R.H., TANSEY	97325791.	FROM N.A.		PRIMATES.	EUKARYOTA; METAZOA;	(HUMAN).	RB 0		NEUR	EPTO	(REL.	(REL.	(REL.		ST	
-	_	444	413	357	5		464		444	21	ING.	RECEPTOR; GLYCOPROTEIN;		G2145080:	BELONGS	O H F	PRODUCTS:	9	LOCATION:		NF S	LATIC	FUNCTION: RECEPTOR		MILI	KECK	¥ M.G.,	•	•		Š	•	AN)	GDNFRB OR TRNR2		BETA RELATED NEUROTROPHIC	R ALI	36,				STANDARD:	
99.6%; 99.4%;	558		_	_			-		_	_					STO	7.					GNAL	NAN	~ FOR	?	MILBRANDT	г						CHORDATA;		R2.		HIC	D AHO	LAST	LAST	CREATED)		ő	
Score Pred.	MW;	d5	g	ğ	정	п	ΉY	RE	ī	g		GPI-ANCHOR;		•	THE	2	A SHC		ATTACHED		ING T	D ACT	NEUR		13 (1	, ZIM	GOLDEN J.P									FACTO	RECUE	ANNO	SEQU	TED)		771	
	MISSING (I 3C74BBFB	GPI - ANCHOR	POTENTIAL.	POTENTIAL.	POTENTIAL.	(POTENTIAL)	HYDROPHOBIC,	RECEPTOR	TGF-BETA	POTENTIAL.		HOR;			GDNFR	PLACENTA	SHORT FO				SIGNALING THROUGH	AUTOPHOSPHORYLATION AND ACTIVATION OF	FOR NEURTURIN.			ZIMONJIC	Д.Р					VERTEBRATA;		٠		FACTOR RECEPTOR 2)	NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA)		SEQUENCE			PRT:	
0;	BEB (IN	HOR R		CAL.	[AL.	(TAL)	OBIC			[AL.		MEMB			REAMILY	NTA	FORM IS		TO THE		THE THE	ON O				σ.	CR CR					BRATA				EPTO	NTNR	N UP	UPDATE)			464	
DB 1; .00e+00	CRC32;	(POTENTIAL).							RELATED			MEMBRANE;			ILY.							THE	MEDIATES				CREEDON D.J.									2	- AL PI	DATE	TE)			8	
••		NTIA					REMOVED									ò	PRODUCED		MEMBRANE			RET	STHE			POPESCU	D. J					TETRAPODA;			•	◛		_					
Length	FORM).						DURING		NEUROTROPHIC			SIGNAL:					D BY		E BY		TYROSINE	RECE				Z Z C	:									FREC	(NRTNR-ALPHA)						
1 464;									DPHIC								ALTE		۾ م		KINASE	PTOR	N-IN			: '						MAMMALIA;				RECEPTOR	Q-ALD						
••							MATURATION		FACTOR								ALTERNATIVE	1	GPT-ANCHOR	Č	ASE	RET RECEPTOR ALSO	NRTN-INDUCED									LIA;				m							
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                                                           -!- TISSUE SPECIFICITY: NEURONS OF THE S
ROOT GANGLIA, AND ADULT BRAIN AND TE
AND IN THE ADRENAL.
-!- ALTERNATIVE PRODUCTS: A SHORT FORM I
SPLICING.
-!- SIMILARITY: BELONGS TO THE GDNFR FAM
EMBL; AF002701; G2145082; -.
MGD; MGI:119462; GFRA2.
RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMB
RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMB
ALTERNATIVE
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                 MEDLINE: 97325791.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
JOHNSON E.M. JR., MILBRANDT J.;
NEURON 18:793-802(1997).

-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV 1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NF
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GDNFR-BETA).
GFRA2 OR GDNFRB OR TRNR2.
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 97325791.
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SUBCELLULAR LOCATION: ATTACHED
SIMILARITY).
TISSUE SPECIFICITY: NEURONS OF
ROOT CANGLIA, AND ADULT BRAIN A
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POTENTIAL.
TGF-BETA RELATED
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  NEUROTROPHIC
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NRTE_CHICK

O13157;

O13157;

T 01-NOV-1997 (REL. 35, CREATED)

T 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

OT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE NEURURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NI

TOTELTOR BETA) (GDNFR-BETA).
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Best Local S
Matches 43
BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
NATURE 387:721-724(1997).

-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INI
AUTOPHOSPHORLATION AND ACTIVATION OF THE RET RECEPTOR
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KING
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KING
RECEPTOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPJ
RECEPTOR; GEZI3305; -.

RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
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SEQUENCE
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LIPID
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CARBOHYD
                                                                                                                                    SEQUENCE FROM
                                                                                                                                                           GALLIFORMES.
                                                                                                                                                                    GALLUS GALLUS (CHIC EUKARYOTA; METAZOA;
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razoa; chordata;
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POTENTIAL.

GPI-ANCHOR (POTENTIAL).

MISSING (IN SHORT FORM).

W; 0A2165C0 CRC32;
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Pred. No. 0.00e+00
19; Mismatches 1
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HYDROPHOBIC,
(POTENTIAL).
POTENTIAL.
                                                                                                                                                                    VERTEBRATA;
                                                                                                                                                                     TETRAPODA;
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                                                                 RET RECEPTOR. ALSO
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                                                                                                                                                                                                              (NRTNR-ALPHA)
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                                                                                                                                                                    AVES; NEOGNATHAE;
                                                                                                              J.
                                    GPI-ANCHOR
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                                                                                                                                                                                                                                             O62997;
O62997;
O1-NOV-1997 (REL. 35, CREATED)

1 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

1 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

E GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF

JE NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).

GFRA1 OR GENFRA OR TRUEL OR RETL1.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRA
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Best Local Similarity 74.7%;
Matches 349; Conservative
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CARBOHYD
CARBOHYD
LIPID
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CHAIN
STRAIN-WISTAR; TISSUE-KIDNEY;
MEDLINE; 97322356.
SANICOLA M., HESSION C.A., WORLEY D.S.,
WALUS L., ROBINSON S., JAWORSKI G., WEI
                                                                                                                                            MEDLINE: 96270513.

JING S., WEN D., YU Y., HOI
ANTONIO L., HU Z., CUPPLES
FOX G.M.;
                                                              SEQUENCE FROM N.A. STRAIN-WISTAR; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                         CELL 85:1113-1124(1996).
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-RETINA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVSPKGPSFQATQAPRVEKTPSLPDDLSDSTSL-GTSVITTCTSVQEQGLKANNSKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YISTCSKEISATEHCSRRKCHKALRQFFDNVPSEYTYRLLFCSCKDQACAEPRRQTIVPF 238
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Pred. No. 0.00e+00;
70; Mismatches 43
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POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR (P
5CA073E4 CR
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NEURTURIN RECEPTOR ALPHA.

HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                    שי
                                                                                                                                                               P.L., I
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                                                                                                                                                             S J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468
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  CARMILLO P., E
H., TIZARD R.,
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HU S.
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AA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
AA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
AA ASAI N., TAKAHASHI M., WOORE M.W., BUJ-BELLO A., DAVIES A.M.,
AASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
ATURE 382:80-83(1996).

1. INTURE 382:80-83(1996).

1. INTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
C. I. SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISCUFIDE-LINTED GDNF DIMER AND WITH 2 MOLECULES OF RET.
C. I. SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
C. I. SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
C. I. SIMILARITY: BELONGS TO THE GDNFR FAMILY.
DR EMBL; U97142; G2320202;
C. RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 22
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PROC. NATL.
[3]
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SEQUENCE
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CARBOHYD
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CARBOHYD
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PROPEP
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 424
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            DSDFGKDGLAGASSHITTKS-MA-APPSCSLSSLPVLMLTALA 457
                                                                                  E--LTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLK-LA
                                 GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKEL-KROOD
                                                      EKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLGSYAGMIGGUUH
                                                                                                                                        ERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYSGLIGTVM
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l Similarity 48.2%;
223; Conservative
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96273032.
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468
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                Score 1554; DB 1; 1
Pred. No. 0.00e+00;
102; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR (POTENTIAL).
G87A2B2A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                               GDNF RECEPTOR I
HYDROPHOBIC, RI
(POTENTIAL).
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94:6238-6243(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA.
                                                                                                                                                                                                                                                                                                                                                                    Length 468;
 463
                                                                                                                                                                                                                                                                                                                                                Indels 18:
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                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT
ID GI
AC PODT 0:

GDNR_MOUSE P97785; 01-NOV-1997 01-NOV-1997

STANDARD;

PRT;

468 AA

(REL

35, 35,

CREATED)

SEQUENCE

UPDATE)

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Best Local
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CARBOHYD
CARBOHYD
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SEQUENCE
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GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (
NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
GFRA1 OR GDNFRA OR TRNR1.
GFRA1 OR GDNFRA OR TRNR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPEP
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                    431
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                                                                                                                                                                                                                                                                                                          16 LMSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO ABOOO800; G1816442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AITTED (FEB-1997) TO EMBL/GENBANK/DDBJ FUNCTION: RECEPTOR FOR GDNF. MEDIATES AUTOPHOSPHORYLATION AND ACTIVATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                   AMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:1100842; GFRA1.
 VIKPNSGPSRARPSAALTVLSVLMLK-LA
                    HITTKS-MA-APPSCGLSSLPVMVFTALA
                                                    FRIKNKPLGPAGSENEIPTHYLPPCANLQAQKLKSNVSGSTHLCLSDNDYGKDGLAGASS
                                                                                                                          DHLCRSRLADFHANCRASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVS
                                       -KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFTE--LTTNIIPGSNK
                                                                                 PWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTNVNVSPKGPSFQATQA-PRVE
                                                                                            PWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPVQTTTAMTTTA
                                                                                                                                                                                                                                                     ALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFR
                                                                                                                                                                                                                                                                                               LOGPELHGWRPPVDCVRANELCAAESNCSSRYRTLROCLAGRDRN-TM---LANK-ECQA
                                                                                                                                                                                                                                                                                                                                         216;
                                                                                                                                                                                                                                                                                                                                                   h 45.1%;
Similarity 48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                  468
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431
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59
347
406
430
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59
406
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                                                                                                                                                                                                                                                                                                                                                                                 51782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-ANCHOR;
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                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.00e+00;
104; Mismatches 111; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                           Score 1527; DB 1,
No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.

GPI-ANCHOR (POTENTIAL).

6C64C182 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROPHOBIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
                   457
 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TGF-BETA RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                            Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                        Gaps
                                        435
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Best Local S
Matches 22
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CARBOHYD
CARBOHYD
CARBOHYD
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SUBSTANTIA NIGRA;
MEDLINE; 96270513.
JING S., WEN D., YU Y.,
ANTONIO L., HU Z., CUPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).

GFRA1 OR GDNFRA OR TRNR1.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOX G.M.;
CELL 85:1113-1124(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDNR_HUMAN
P56159;
                                                                                                                                                                                                                                                                                                                                                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS MIM; 601496; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR;
                                                                                       247
   367
                                            307
                                                                                                                                 187
                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTOPHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                             TSVS-NDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSY....
                                                                                                                                                                                      APPVQTTTATTTTALRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLC::S
                                                                                                                                                                                                                     TM---LANK-ECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTHGHID TELL
   GPSFQATQAPRV-E-
                                           PNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTNVNVS; K
                                                       PNYIDSS-S-LSVAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGSDV1Vw.:
                                                                                       EKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLGSYAGMI (****);
                                                                                                  EKPNCL-LQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGIVMI
                                                                                                                                 REISPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYEDK
                                                                                                                                                                           PYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSY'SF:
                                                                                                                                                                                                                                   SLASGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQS;-(UNIV
                                                                                                                                                                                                                                                               FIDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAESNCSSRYRTLKQCLAGGAGG
                                                                                                                                                                                                                                                                                                           223;
                                                                                                                                                                                                                                                                                                                      Similarity
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405
428
464 AA;
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429
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59
59
7
346
7
405
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428
6
51291 MW;
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464
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  -KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFJ
                                                                                                                                                                                                                                                                                                                      44.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                         ; Score 1521;
; Pred. No. 0.
100; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNF. MEDIATES D ACTIVATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE GDNFR FAMILY
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POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                     GPI-ANCHOR
2C8C3574
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HYDROPHOBIC, REMOVED
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                           Mismatches 121;
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                                                                                                                                                                                                                                                                                                                      DB 1;
00e+00;
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
CRC32;
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THE RET RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                REMOVED
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HU S., Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                              Length 464;
                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                MATURATION
                                                                                                                                                                                                                                                                                                           18:
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ELITNIIP-GSNKVIKPNSGPSRARPSAALTVLSVLMLKLAL

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S--LGT-SVITTCTSVQEQGL-KANNSKELSMCFTE--LTTNIIPG-SNKVIKP-NS-G-

443

454

NGNYEKEGLGASSHITTKS-MA-APPSCGLSPLLVLVVT-AL

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Best Local S
Matches 22
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LIPID
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CARBOHYD
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013156;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS
EMBL; U90541; G2213803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.; NATURE 387:721-724(1997).

-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALLUS GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFRA1 OR GDNFRA.
    333
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                                                                                                                                          264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTOPHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDCVKASDQCLKEQSCSTKYRTLRQCVAGKESNFSRATGLEAKDECKSAMEALKQKSLYN 89
                                                                                                                    VDCVRANELCAAESNCSSRYRTLRQCLAGRD----RNTMLANK-ECQAALEVLQESPLYD 92
PKHSYGMLFCSCRDVACTERRRQTIVPVCSYEDREKPNCLNLQESCKKNYICRSRLADFF 263
                                                                                                                                                                                                                                                                       VVSAKSNHCLDAAKACNINDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFDRVP 212
                                                                                                                                                                                                                                                                                                       VLS-KGNNCLDAAKACNLNDTCKRFRSAYITPCTSSTS-NEICNKRKCHKALRLFFDKVP 203
                                                                                                                                                                                                                                                                                                                                                                        CRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGADP 152
                                                                                                                                                                                                                                                                                                                                                                                                   CRCKRGMKKEKNCLRIYWSMYQSL-OGNDLLEDSPYEPVNSRLSDIFRLAPIVS----VEP 145
                                                                                                                                                                                     SEYTYRMLFCSCQDQACAERRRQTILPSCSYEDKEKPNCLDLRGVCRTDHLCRSRLADFH
                                                                                            ANCRASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224; Conservative
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1 27
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163
163
346
405
430
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62
163
346
405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPI-ANCHOR; MEMBRANE; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDNF. MEDIATES THE GDNF-INDUCED ACTIVATION OF THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1501; DB 1;
Pred. No. 0.00e+00;
92; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
GPI-ANCHOR
C8D241C9
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POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 469;
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01-OCT-1996 (REL. 3
15-JUL-1998 (REL. 3
ELONGATION FACTOR T
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01-OCT-1996
15-JUL-1998
                                                                     NP_BIND
NP_BIND
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                           CHAIN
                                                                                                                                                                                                                         BIOSYNTHESIS.
-I- SUBCELLULAR LOCATION: MITOCHONDRIAL.
EMBL; L38995; G704416; -.
EMBL; X84994; G899285; -.
EMBL; X84694; G899285; -.
EMBL; S75463; G833999; ALT_INIT.
                                                                                                                                                                                                                                                                                     SUBMITTED (MAR-1996) TO THE SWISS-PROT DATA BANK.
-I- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 95129693.
WELLS J., HENKLER F., LEVERSHA M., FEBS LETT. 358:119-125(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTU_HUMAN P49411;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBINSON B.H.;
GENE 197:325-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-KIDNEY, AND HEART;
MEDLINE; 97473528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORIAX V.L., BURKHART W.A., SPREMULLI L.L.,
BIOCHIM. BIOPHYS. ACTA 1264:347-356(1995).
                                                                                                                                                                                                    MIM; 602389;
                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; PRIMATES
                                                                                                                                                         TRANSIT
                                                                                                                                                                                ELONGATION FACTOR;
                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                 HSC-2DPAGE; P49411; HUMAN
                                                                                                                                                                                                                                                                                                                          DONN M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING M., MERANTE F., CHEN H.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96138557.
                                                                                                                                                                   CRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443
231 LGLKSVQKLLDAVDTYIPVPARDLEKPFLLPVEAVYSVPGRGTVVTGTLERGILKKGDEC 290
                                                                                                                                                                                                                                                                                                                                      SSUE-HEART;
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                      Similarity 27.6%;
21; Conservative
                                                                                                                                                                             PS00301; EFACTOR_GTP;
ON FACTOR; PROTEIN BIO
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                                                                                                                                                                   GTP-BINDING
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34, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
TU, MITOCHONDRIAL PRECURSOR
                                    3.0%;
27.6%;
                                                                      49541 MW;
                                                                 MITOCHONDRION.
ELONGATION FACTOR TU.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
MISSING (IN REF. 3).
D -> N (IN REF. 1).
WY: F29C75C5 CRC32;
                                                                                                                                                                             BIOSYNTHESIS; MITOCHONDRION;
                       Score 100; DB 1; L
Pred. No. 3.18e-02;
19; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; TETRAPODA;
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                       Indels
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LGLTEGEEFYEA-SPYEPVTSR-LSDIFRLA--SIFSGTGADPVVSAKSNH-CLDAAKAC

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RESULT
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NOV_MOUSE Q64299; 01-NOV-1997 01-NOV-1997 01-NOV-1997

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(REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)

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l. No. 9.87e-
Mismatches
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SIMILARITY
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.87e-03;
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DOMAIN
DOMAIN
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ONCOGENE 12:1479-1492(1996).
-i- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
GROWTH REGULATION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY. CEP-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
-i- SIMILARITY: CONTAINS 1 VWFC DOMAIN
-I- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBG INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FU AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL F
                                                                                                                          Q10792;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UP
01-0CT-1996 (REL. 34, LAST ANNOTATION
50S RIBOSOMAL PROTEIN L19.
RPLS OR MTCY274.35C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00222: IGF_BINDING: 1.
PROSITE: PS01185: CTCK_1: 1.
PROSITE: PS01205: CTCK_2: 1.
PROSITE: PS01208: VWFC: 1.
PROTO-ONCOGENE: GROWTH FACTOR BII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X97863; E1181580; -
EMBL; Y09257; E281106; -
EMBL; X96585; E228599; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-129/SV, AND ICR: TISSUE-BRAIN;
SNAITH M.R., NATARAJAN D., TAYLOR L.B., CHOI C.P., MI
PERBAL B., SCHOFIELD P.N., BOULTER C.A.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                      MYCOBACTERIUM TUBERCULOSIS PROKARYOTA; FIRMICUTES; AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA;
                                                                    STRAIN-H37RV;
                                                                                SEQUENCE
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                                                                                                                                                                                                                                                      260 KCLRTKKSLKAIHLQFENCTSLYTYKPRFCGVCSDGRCCTPHNTKTI
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17; Conser
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                                                                                                    ACTINOMYCETALES; MYCOBACTERIACEAE
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Pred.
10; M
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9.98e-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                            Length 354;
                                                                                                                                                                                                                                                                                        Indels
                       AND FUNCTION
                                                                                                                                                                                                                                                                 306
                                                        WALSH S.V.;
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P13945;
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 274024; E248891; -.
PROSITE; PSO1015; RIBOSOMAL_L19;
RIBOSOMAL PROTEIN.
SEQUENCE 113 AA; 13013 MW; 91
                                                                                                                                                                                                                                      RUIZ J., :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
BETA-3 ADRENERGIC RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS, SEQUENCE FROM N.A. MEDLINE; 93279311.
VAN SPRONSEN A., NAHMIAS C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMORINE L.J., MARULLO S., BR
DELAVIER-KLUTCHKO C., STROSB
SCIENCE 245:1118-1121(1989).
                                                       ENDOCRINOLOGY 137:2638-2641(1996).
-IF FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND PROTEINS.
                                                                                                        CANDELORE M.R.,
STRADER C.D.;
                                                                                                                                                                MEDLINE; 96361936.
FUJISAWA T., IEGAMI H., YAMATO E., T
HAMADA Y., OGA T., UEDA H., SHINTANI
DIABETOLOGIA 39:349-352(1996).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 392-408 FROM N.A. MEDLINE; 93125503.
GRANNEMAN J.G., LAHNERS K.N.,
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93285320.
LELIAS J.M., KAGHAD M., RODRIG DUPRE I., DELPECH B., BENSAID FEBS LETT. 324:127-130(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 89368947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN)
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                                                                                                                                                                                                               VARIANT ARG-64.
                                                                                                                                                                                                                                                           CLEMENT K., VAISSE C.,
                                                                                                                                                                                                                                                                        VARIANT ARG-64.
                                                                                                                                                                                                                                                                                                                                                                                                                             EUR. J. BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STROSBERG A.D.,
                                                                                                                                 MEDLINE;
                                                                                                                                           VARIANT ARG-64
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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THERMOGENESIS.

1 SUBCELLULAR LOCATION: INTEG
1 TISSUE SPECIFICITY: MAINLY
1 POLYMORPHISM: THE VARIANT A
WEIGHT GAIN (OBESITY) AND T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U
                                                                                                                                                                                                                                                                                               PHARMACOL.
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12; Conser
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larity 46.2%;
Conservative
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                                                                                                                                                                                                                                                                                              LAHNERS K.N., RAO 42:964-970(1992).
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. 213:1117-1124(1993).
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STROSBERG
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JENSAID M.,
  N: INTEGRAL MEMBRANE PROTEIN.
MAINLY IN ADIPOSE TISSUES.
ARTANT ARG-64 SEEMS TO BE ASSOCIATED
Y) AND TO IS ALSO ASSOCIATED WITH
                                                                                                                    TOTA L.M.,
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OSBERG A.D.;
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Pred. No. 2.
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P25793;
01-MAY-1992
01-MAY-1992
01-MOV-1995
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PRATT D., COX G.N., MILHAUSEN M.J., BOISVENUE R.J.;

MOL. BIOCHEM. PARASITOL. 43:181-192(1990).

NOL. BIOCHEM. PARASITOL OF THE PROTEASE CORRELATES WITH BLOOD-FEEDING FUNCTION: EXPRESSION OF THE PROTEASE IN BLOOD DIGESTION.

1- DEVELOPMENTAL STAGE: AT LOW LEVEL IN THE THIRD AND FOURTH-STAGE LARVAE, AND ABUNDANT IN ADULT WORMS.

1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.

1- SIMILARITY: STRONGEST, TO CATHEPSIN B.
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CARBOHYD
DISULFID
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01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE)
CATHEPSIN B-LIKE CYSTEINE PROTEINASE 2 PRECURSOR
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G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRA
MULTIGENE FAMILY; PHOSPHORYLATION; LIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
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13; Conservative
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METAZOA; ACOELOMATES;
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CYTOPLASMIC (POTENTIAL)
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Pred. No.
10; Misma
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PALMITATE (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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TEIN; PALMITATE;
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R PIR; A44965, A44965.

JR HSSP; P07858; 1HUC.

DR PROSITE; PS00639; THIOL_PROTEASE_IS; 1.

PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.

PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
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P19092;
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EUKARYOTA; METAZOA; P
                                                                                                                                                                                                                                 CATHEPSIN
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                                                                                                                                                                                                                                                                                                            200 TYYGEC-RGTAPTPPC-KRKCRPGVRKMY-RIDKRY 232
                                                      YDROLASE;
                                                                                                                                                                                                                                                                                                    180 SYISICNREISPTERCNRRKCHKALRQFFDRVPSEY 215
                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                Similarity
12; Conser
                                                           PS00139; THIOL_PROTEASE_CYS; PS00639; THIOL_PROTEASE_HIS; PS00640; THIOL_PROTEASE_ASN;
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990 (REL.
995 (REL.
9-LIKE C
                                              FAMILY
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305
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147
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larity 33.3%;
Conservative
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                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                               . 16, CREATED)
. 16, LAST SEQUENCE UPDATE)
. 32, LAST ANNOTATION UPDATE)
CYSTEINE PROTEINASE 1 PRECURSOR (EC
                                                     PROTEASE;
96
342
342
114
285
305
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152
218
205
205
138
198
198
                                                                                                                                                                                                           ACOELOMATES;
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                                                     ZYMOGEN;
ACTIVATION PEPTIDE (PACTIVATION PEPTIDE (PCYSTEINE PROTEINASE 1
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred.
9; M
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ACTIVATION PEPTIDE (FACTIVATION PEPTIDE (FACTIVATION PROTEINASE 2 BY SIMILARITY.

POTENTIAL.

POTENTIAL.
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89092341 CRC32;
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                           NEMATODA;
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No. 8.96e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YS; 1.
IS; 1.
SN; 1.
GLYCOPROTEIN; 9
                                                     GLYCOPROTEIN;
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                                                                                                                                                                                                                                                                                                                                              Length 342;
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                                                     SIGNAL:
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Best Local Similarity 32.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%; Score 91; DB 1; Len Best Local Similarity 33.3%; Pred. No. 8.96e-01; Matches 12; Conservative 9; Mismatches 12;
                                                                                                                                       CARBOHYD
CARBOHYD
SEQUENCE
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DISULFID
DISULFID
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CARBOHYD
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ACT_SITE
CARBOHYD
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ASP2_BLAGE
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLLINE; 95370299.
ARRUDA L.K., VAILES L.D., MANN B.J., SHANNON J., FOX J.W.,
VEDVICK T.S., HAYDEN M.L., CHAPMAN M.D.;
J. BIOL. CHEM. 270:19563-19568(1995).
-!- FUNCTION: MAJOR ALLERGEN; FUNCTIONS AS A DIGESTIVE ENZYME IN THE
                                                                                                                                                                                                                                                                                                                                                                                                P54958;

01-OCT-1996 (REL. 34, CREATED)

01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

01-OCT-1997 (REL. 35, LAST ANNOTATION UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

ASPARTIC PROTEASE BLA G 2 PRECURSOR (EC 3.4.23.-) (ALLERGEN BLA G II).

BLATTELLA GERMANICA (GERMAN COCKROACH).

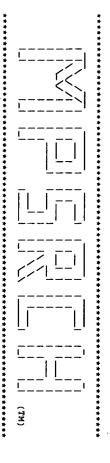
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; BLATTODEA.
                                                                                                                                                                                                                        HYDROLASE; ASPARTYL PROTEASE; SIGNAL 1 7 PROPEP 7 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                              -
 182
                                            123 YEASPYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKAC-NLNDNCKKLRSSY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SYISICNREISPTERCNRKCHKALRQFFDRVPSEY 215
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                       89
                                                          34 FINTQYAGITKIGNQNF-LT-VFDSTSCN-VVVA-SQECVGGACVCPNL-QKYEKLKPKY 88
                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; EUKARYOTIC ASPARTYL PROTEASES FAMILY.
IS 183
                       IS 90
                                                                                                                                                                                                                                                        U28863; G1176397; -.
TE; PS00141; ASP_PROTEASE; FALSE_NEG.
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340
PA;
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                                                                                                                                       1128 B
214 B
2156 B
2159 B
205 B
205 B
205 P
1138 P
1138 P
296 P
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POTENTIAL.
                                                                                         Score 91; DB 1; Length 352; Pred. No. 8.96e-01; 16; Mismatches 20; Indels
                                                                                                                                                                                               SIGNAL; ALLERGEN; ZYMOGEN. POTENTIAL. REMOVED IN MATURE FORM. ASPARTIC PROTEASE BLA G 2. BY SIMILARITY.
                                                                                                                                       POTENTIAL.
23F3B608 CRC32;
                                                                                                                                                                         BY SIMILARITY. POTENTIAL.
                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 AA
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Search completed: Mon Mar Job time : 51 secs.

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14:06:44 1999

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:53:57 1999; MasPar time 17.15 Seconds 779.553 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-866-354-43 (1-498) from US08866354.pep 2337 1 MYXXLXXXPXPPXXXMXLXL.....XLPVLMLTALAXLLSXXXXS 498

Scoring table: РАМ 150 Gap 11

Searched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 1:swissprot

Statistics: Mean 45.078; Variance 68.218; scale 0.661

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
11111111111111111111111111111111111111	NO.
1803 1778 1778 1772 1775 1759 1551 100 100 100 100 100 100 100 93 93 93 93	Score
7777788 70000080444444444466 7008048000444667	Query
468 464 463 4664 4664 4652 2524 2871 2871 3871 3871 3051 427 816 816 816 816 816 816 816 816 816 816	Length
	DB
GDNR_RAT NRTR_HUMAN NRTR_MOUSE GDNR_MOUSE GDNR_HOUSE GDNR_CCHICK NRTR_CHICK NRTR_CAEEL YBHC_ECOLI NEL_MOUSE YNX3_CAEEL YBHC_ECOLI NEL_RAT LDLR_RAT LDLR_RAT LDLR_RAT SLIT_DROME NTCL_HUMAN ALBU_RANCA DLK_HUMAN	ID
GDNY RECEPTOR ALPHA PR NEURTURIN RECEPTOR ALP GDNY RECEPTOR ALPHA PR REURTURIN 1 PRECURSOR FIBRILLIN 1 PRECURSOR ESTRADIOL 17 BETA-DEHY FIBRILLIN 1 PRECURSOR CESTRADIOL 17 BETA-DEHY FIBRILLIN 1 PRECURSOR MEDROSTICAL PROTEIN T HYPOTHETICAL PROTEIN T HYPOTHETICAL FROTEIN T HYPOTHETICAL FROTEIN T HYPOTHETICAL FROTEIN PRECURSOR HYPOTHETICAL SG. 3 KD P NEL PROTEIN PRECURSOR HYPOTHETICAL SG. 3 KD P NEL PROTEIN PRECURSOR NEUROGENIC LOCUS NOTCH SERUM ALBUMIN (FRAGMEN DELTA-LIKE PROTEIN PRE DELTA-LIKE PROTEIN PRE DELTA-LIKE PROTEIN PRE	Description
0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.55e-00 186e-00 1.98e-03 1.98e-03 1.98e-01 1.98e-01 1.98e-01 1.98e-01 1.98e-01	Pred. No.

ALIGNMENTS

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DR EMBL; U97440; G139903; T. DR EMBL; U97142; G228022; T. KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; FT SIGNAL 24 POTENTIAL.	-!- SUBUNIT: 2 MOLECULES OF GOMER-ALPHA ARE WITH THE DISULFIDE-LINKED GDNF DIMER AND -!- SUBCELLULAR LOCATION: ATTACHED TO THE ME -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, -!- SIMILARITY: BELLONGS TO THE GDNFR FAMILY.	PHILLIPS H.S. ASAI N., TAKA NATURE 382:80 -1- FUNCTION: AUTOPHOSP	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243, (3) SEQUENCE FROM N.A. MEDLINE; 96273032. TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., BECK C.D., GRAY C., ARMANINI M.P., POLLOCK	CELL 85:1113-1124(1996). [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-WISTAR; TISSUE-KIDNEY; MEDLINE; 97322356. MEDLINE; 97322356. WALUS L., ROBINSON S., JAWORSKI G., WEI H., PEPINSKY R.B., CATE R.L.;	EUTHERIA; RODENTIA. [1] [1] [1] [2] [1] [1] [2] [1] [1] [2] [1] [2] [2] [2] [2] [2] [2] [2] [2] [2] [2	GDNR_RAT STANDARD; PRT; 468 AA. 062997; O1-NOV-1997 (REL. 35, CREATED) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND GFRA1 OR GDNFRA OR TRNR1 OR RETL1. RATTUS NORVEGICUS (RAT).
RANE; SIGNAL.	RE THOUGHT TO FORM A COMPLIX AND WITH 2 MOLECULES OF RET. E MEMBRANE BY A GPT-ANCHOR. ER, BRAIN AND KIDNEY.	JJ-BELLO A., DAVIES A.M., ISON C.E., ROSENTHAL A.: THE GDNF-INDUCED THE RET RECEPTOR.	3(1997). , STONE D.M., POULSEN K.T K R.A., HEFTI F.,	CARMILLO P., EHRENFELS C., H., TIZARD R., WHITTY A.,	TETRAPODA; MAMMALIA; ., FANG M., TAMIR R., ., HU S., ALTROCK B.W	(TGF-BETA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                         GFRA2 OR GDNFRB OR TR
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                             NRTR_HUMAN STANDARD; PRT; 464 AA.
000451;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA)
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE FROM N.A.

MEDILINE; 97325791.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,

JOHNSON E.M. JR., MILBRANDT J.;

NEURON 18:793-802(1997).

PEUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED

AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO

TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE

RECEPTOR.

PRECEPTOR.

1- SUBGELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHO

SIMILARITY).
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SEQUENCE
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PROPEP
                                                                                                                                                                                                       GDNFR-BETA)
                                                                                                                                                                                                                                                                                                                                          436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEDSPYEP-VNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAY
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                                                                                                                                                                                                                                                                                                                                                       KSNVSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MXLXLLSLALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXXRTLRQCXAGXXX 75
                                                                                                                                                                                                                                                                                                                                                                                                       DVTMWQPA--P--PVQTTTATTTTAFRVKNKP-LGPAGSENE-IPTHVLPPCANLQAQKL 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITPCTTSMSN-EVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCR--DIACTERRRQTIVP
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255; Conser
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468
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59
347
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53.3%;
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Pred. No. 0.00e+00;
23; Mismatches 18;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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HYDROPHOBIC, REMOVED
(POTENTIAL).
                                                                                                                                                                    VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 183;
                                                                                                                                                                    TETRAPODA;
                                                                                                                                                                                                                  (GDNF RECEPTOR BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DURING
            BY A GPI-ANCHOR
                                                                                                                                                                    MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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            (BY
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RA SHAMAN
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Best Local S
Matches 26
                                                                                                           NRTR_MOUSE STANDARD; PRT; 463 AA.
008842;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA)
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                              GFRA2 OR GDNFRB OR T
MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED SPLICING IN BOTH BRAIN AND PLACENTA.
-i- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
EMBL; AF002700; G2145080; -.
            SEQUENCE FROM N.A. MEDLINE; 97325791.
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VARSPLIC
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CHAIN
  BALOH
                                                     EUTHERIA;
                                                                                                      (GDNFR-BETA)
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                                                                                                                                                                                                                                                     XXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLT-AL
                                                                                                                                                                                                                                                                        SMCFTELTINIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLKQAL
                                                                                                                                                                                                                                                                                                                      --PSF-----QA-TQAPRVEKTPSLPDDLSDSTSLGTSVITTCTSVQEQGLKANNSKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLASPSSLQGPELHGW-RPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRNTMLAN-K
 R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 76.5%;
Similarity 56.2%;
262; Conservative
                                                     RODENTIA
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 TANSEY
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                                                                                         TRNR2
 M.G.,
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 GOLDEN
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POTENTIAL.
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POTENTIAL.
GPI-ANCHOR (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
MISSING (IN SHORT FORM)
M; 3C74BBFB CRC32;
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Pred. No. 0.00e+00;
17; Mismatches 166;
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TGF-BETA R
RECEPTOR 2
                                                                 VERTEBRATA;
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 J.Р.,
 CREEDON
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                                                                 TETRAPODA;
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  GDNR_MOUSE
P97785;
01-NOV-1997
01-NOV-1997
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LIPID
VARSPLIC
SEQUENCE
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CARBOHYD
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EMBL; AF002701; G2145082; -.
MGD; MGI:1195462; GFRA2.
RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE;
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                                                                                                                                              XXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLTALA
                                                                                                                                                                                                                                                                   --PTFS----A-TQAPRVEKTPSLPDDLSDSTSLGTSVITTCTSIQEQGLKANNSKEL 418
                                                                                                                                                                                                                                                                                                                                     NYVDSNPTGIVVSPWCNCRGSGNMEEECEKFLKDFTENPCLRNAIQAFGNGTDVNMSPKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-----CQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLASPSSPQGSELHGW-RPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRNTMLAN-K 76
                                                                                                                                                                                    SMCFTELTTNISPGSKKVIKLYSGSCRARLSTALTALPLLMVT-LA
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1 Similarity 56.0%;
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  SEQUENCE
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GPI-ANCHOR (POTENTIAL)

MISSING (IN SHORT FORM
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                                                               PRT;
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    UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (
REUROJROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
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TISSUE-DORSAL ROOT GANGLION.
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SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT
WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                             | LIGTVMTPNYIDSS-SLS-VAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGS
                                                                                                                                                                                                                                                     LEDSPYEP-VNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFSLTSGLEAKDE--CRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDL 115
                                       KSNVSGSTHLCLSDNDYGKDGLAGASSHITTKSMAAPPSCGLSSLPVMVFTALAALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTXLASGXEXXXXXXCXXAXEXLXXSSLXDCRCKRGMKKEXXCLXIYWSXHXXLXXGNXX 135
  KXNXSXEXXXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLTALAXLLS
                                                                                   DVTMWQPA--P--PVQTTTAMTTTAFRIKNKP-LGPAGSENE-IPTHVLPPCANLQAQKL
                                                                                                                                                                     LIGTXMTPNYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGX
                                                                                                                                                                                                                                                                                                                                                                                                                            MXLXLLSLALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.8%;
Similarity 51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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59
347
406
430
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468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPI-ANCHOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1772; DB 1; 1
Pred. No. 0.00e+00;
29; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
THR-RICH.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR (P
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GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROPHOBIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C64C182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TGF-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY A GPI-ANCHOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO FORM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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Best Local S
Matches 25
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CARBOHYD
CARBOHYD
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LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOX G.M.;
CELL 85:1113-1124(1996).
-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES
-I- FUNCTION-PHORYLATION AND ACTIVATION OF
                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-SUBSTANTIA NIGRA;
MEDLINE; 96270513.
JING S., WEN D., YU Y., HOLST F
ANTONIO L., HU Z., CUPPLES R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA
NEUROTTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; PRIMATES.
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P56159;
                    349
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 376
                                        316
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                                                                               256
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                                                                                                                                                                                                                                                    1 MFLATLYFALPLLDLLLSAEVSGGDRL--DCVKASDQCLKEQSCSTKYRTLRQCVAGKET
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SIMILARITY: BELONGS
1; 601496; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE 1 WITH THE DISULFIDE-LINKED GDNF DIMER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                                                                            SIMILARITY)
                                    LIGTXMTPNYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGX
                                                   LIGTVMTPNYIDSS-SLS-VAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGS
                                                                                                                                                                       LEDSPYEP-VNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAY
                                                                                                                                                                                                  DVTVWQPA--P--PVQTTTATTTTALRVKNKP-LGPAGSENE-IPTHVLPPCANLQAQKL
                                                                                                                     IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXP
                                                                                                                                ITPCTTSVSN-DVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCR--DIACTERRRQTIVP
                                                                                                                                                             NFSLASGLEAKDE--CRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDL 115
                                                                                                                                                                                                                                          MXLXLLSLALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXXRTLRQCXAGXXX
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                 361
59
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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59
346
405
428
51291
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                                                                                                                                                                                                                                                                                                                                                                                                                          GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                 Score 1758;
Pred. No. 0.0
24; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                               THE GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                            GDNF RECEPTOR ALPHA. HYDROPHOBIC, REMOVED
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOUIS
                                                                                                                                                                                                                                                                                                                          2C8C3574
                                                                                                                                                                                                                                                                                 Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464
                                                                                                                                                                                                                                                                                            DB 1;
.00e+00;
                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THOUGHT TO FORM
D 2 MOLECULES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANG M., TAMIR
HU S., ALTROCK
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A COMPLEX
RET (BY
                                                                                                                                                                                                                                                                                 Gaps
                                     375
                                                                                                                                                                               174
                  402
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Best Local S
Matches 23
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
CHAIN
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
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BUJ-BELLO A., ADU J., PINON L.
ROSENTHAL A., CHINCHETRU M., B
NATURE 387:721-724(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROTROPHIC FACTOR RECEPTOR 1). GFRA1 OR GDNFRA.
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                                     230
                                                                           195
                                                                                                                173
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 255
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L; U90541; G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: 2 MOLECULES OF GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR GDNF. MEDIATES AUTOPHOSPHORYLATION AND ACTIVATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                       PVCSYEDREKPNCINIQESCKKNYICRSRIADFFTNCQPESRSVSSCIKENYADCIIAYS
                                                                     LLEDSPYEP-VNSRLSDIFRLAPIVSV---EPVLS-KGNNCLDAAKACNLNDTCKRFRSA
                                                                                                                                                                                                                           NTXLASGXEXXXXXCXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGNX 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                        MXLXLLSLALPLXXXLQGAELXGXXRLXX-DCVXAXXXCXAEXXCSXXYRTLRQCXAGXX
                                                                                                                                                                                                                                                                                                                                            MFLALLYLALPLADVILSAEVSGLPGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKE
                                                                                                                                                  SNFSRATGLEAKDE--CKSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETS
 PSCSYEXXEKPNCLDLRXXCRTDXLCRSRLADFXTNCXXXXRXVXSCXAXNYXXCLXAYX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSNVSGNTHLCISN-GNYEKEGLGASSHITTKSMAAPPSCGLSPLLVLVVTALSTLLSLT
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              469
                                                                                                                                                                                                                                                                                                                                                                               68.4%;
larity 49.3%;
Conservative
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62
163
346
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163
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52043
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469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Œ;
                                                                                                                                                                                                                                                                                                                                                                                 Score 1599; DB 1;
Pred. No. 0.00e+00;
31; M1smatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDNFR-ALPHA ARE 1
ED GDNF DIMER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BUCHMAN V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNF RECEPTOR ALPHA. HYDROPHOBIC, REMOVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8D241C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
CRC32;
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THE RET RECEPTOR
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D WITH 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THOMPSON
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314
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Best Local S
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.; NATURE 387:721-724(1997).

-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPT TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE K RECEPTOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A -I- SIMILARITY: BELONGS TO THE GDNFR FAMILY.

EMBL; U90542; G2213805; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRTR_CHICK STANDARD; PRT; 465 AA.
013157;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA)
RECEPTOR BETA) (GDNFR-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFRA2 OR GDNFRB.
GALLUS GALLUS (CHICKEN)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR;
                                                                                        144
                                                                                                                                     131
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                                          188
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                                                                                                                                                                                                                                                                        ALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXXNTXLASGX 83
                                                                                                                                                                                                                                                                                                                SLAAPPSPPGQDLQGW-RVPVDCIRANKLCAAEGSCSSRYRTLRQCLAGRDRNTMLAN-K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRKSNESVDTELCLNENAIGKDNTPGVSTSHISSENSFALPTSFYPSTPLILMTIALSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLIGTVMTPNYIDSS-SLS-VAPWCDCSNSGNDIDECRKFLNFFQDNTCLKNAIQAFGNG
                          SATEHCSRRKCHKALRQFFDNVPSEYTYRLLFCSCK--DQACAEPRRQTIVPFCSYEDKE
                                                                                                           -ITSRLSDIFRLASIFSGM--DPATNSKSNHCLDAAKACNLNDNCKRLRSGYISTCSKEI
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SXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEXXE
                                                                                        EXXXXXXCXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGNXXLEXSPYEP
                                                                                                                                                                                                     E-----CQAALEYLQESPLYDCRCKRGMRKEIQCLQVYWSIHLGLAEGEEFYEASPYEP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDVNVWQ-----PILPVQTTTATTTTASRLKNTGS-ETTNNEIPT-HND-SPACANLQAQK
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223; Conser
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387
412
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465
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larity 47.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                              Score 1561; DB 1; 1
Pred. No. 0.00e+00;
44; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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POTENTIAL.
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5CA073E4
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NEURTURIN RECEPTOR ALPHA.
HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S THE NRTN-INDUCED
RET RECEPTOR. ALSO
TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                           Length 465;
                                                                                                                                                                                                                                                                                                                                                                  Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVES;
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263
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HSSP: P20593; 1ESL.

PROSITE; PS00010; ASX_HYDROXYL; 23.

PROSITE; PS00002; EGF_1; 34.

PROSITE; PS01186; EGF_2; 29.

PROSITE; PS01187; EGF_CA; 21.

DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF-LIKE

TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN

-- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

-- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

-- SIMILARITY: CONTAINS 6 ANK REPEATS.

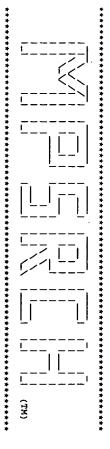
-- SIMILARITY: CONTAINS 6 ANK REPEATS.
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P21783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (REL. 18, CREATED)
01-CCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 90385285.
COFFMAN C., HARRIS W., KINTI
SCIENCE 249:1438-1441(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CINTNER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 1759-1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPNCLDLRNVCRADHLCRSRLADFHANCQASFQSLTSCPGDNYQACLGSYTGLIGFDMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXCFXE--LTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSPPITMLPKVEK-SPA--L---PD-DINDSNTMY-DTSIITTCTSIQEHGQKLNKSKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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2524
1728
1750
2524
2524
99
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                                                                                                                                                                      CYTOPLASMIC EGF-LIKE 1. EGF-LIKE 2.
  THE BOST-LIKE EGF-LIKE EGF-LIKE
                                                                                                                                                                                                                                 POTENTIAL.
NEUROGENIC
                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                      EXTRACELLULAR
                                                                                   E 4.
E 5, CALCIUM-BINDING E 6.
E 6. CALCIUM-BINDING E 7, CALCIUM-BINDING E 8, CALCIUM-BINDING E 9, CALCIUM-BINDING
                                                                                                                                                                                                                                  LOCUS NOTCH PROTEIN
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
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                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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DOMAIN
DO
           EGF-LIKE 17.
EGF-LIKE 18, CL
EGF-LIKE 19, CL
EGF-LIKE 20, CL
EGF-LIKE 21, CL
EGF-LIKE 23, CL
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 8 15:06:23 1999; MasPar time 16.71 Seconds 785.287 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 1:swissprot

Statistics: Mean 43.671; Variance 63.739; scale 0.685

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

NRTILMONSE STANDARD; PRT; 463 AA. O08642; O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) STANDARD REDEFOR ALPHA PRECURSOR (NTNR-ALPHA) (NTNR-ALPHA) (TGF- BETA RELATED NEUROTORDHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA) GDNFR BETA). GERA2 OR GOMFRB OR TRNR2. WIS MUSCULUS (MOUSE). EUKRAYOTA, MERA20A: CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA: EUTHERIA: RODENTIA. [1] BALOH R.H. TANNSFY M.G., GOLDEN J.P., CREEDON D.J., HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; NEURON 18:793-802(1997). -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED JOHNSON E.M. JR., MILBRANDT J.; NEURON 18:793-802(1997). -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED JOHNSON E.M. JR., MILBRANDT J.; NEURON 18:793-802(1997). -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED JOHNSON E.M. JR., MILBRANDT J.; NEURON 18:793-802(1997). -1- SUBCELLULAR LOCATION: ATTACHED TO THE RET RECEPTOR. ALSO-/AS: JOHNSON E.M. JR., MILBRANDT J.; NEURON 18:793-802(1997). -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR: (ASSULAND AUTOROSPHORLATION AND ACTIVATION OF THE SUPERIOR CERVICAL AND DORSAL RECEPTOR: GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPILEIN AND IN THE ADREMAL. -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY. EMBL: AF002701: G2145082; - NEURO META AND AUTOROSPOTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL: AND IN THE ADREMAL. -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY. EMBL: AF002701: G2145082; - POTENTIAL. CARBOHYD 57 93 57 POTENTIAL CARBOHYD 57 93 57 POTENTIAL CARBOHYD 57 93 57 POTENTIAL CAR	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	366666666666	CCCCFFFFF	RESULTION NO.
ANDARD; PRT; 463 AA. 35, CREATED) 36, LAST SEQUENCE UPDATE) 36, LAST SEQUENCE UPDATE) 36, LAST SEQUENCE UPDATE) 36, LAST ANNOTATION UPDATE) 37, LAST SEQUENCE UPDATE) 38, CARECURSOR (NYENRALPHA) (NRTHR-ALPHA) (OTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETTENAPODA: MAMMALIA; 35) R TRNR2. SE). R TRNR2. SE). R TRNR2. SE). A.: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA; A: CHORDATA: VERTEBRATA: TETRAPODA: MATURIA A: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA: TETRAPODA: MATURIA A: CHORDATA: VERTEBRATA: TETRAPODA: MATURIA A: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA: TETRAPODA: MATURIA A: CHORDATA: VERTEBR	SIGNAL CHAIN PROPEP CARBOHYD CARBOHYD CARBOHYD LIPID VARSPLIC SEQUENCE	-!- SUBCEPTO SUBCEPTO SUBCEPTOR AND IN -!- SUBCEPTOR AFOO MGD: I. SECEPTOR AFOO MGD; MGD; MGD; MGD; MGD; MGD; MGD; MGD;	SEQUENCE FI MEDLINE; 9 MEDLINE; 9 MEDLOH R.H. HEUCKBROTH JOHNSON E: NEURON 18: -1- FUNCTIONED AUTOPHOTO MED	NRTR_MOUSE OO8842; O1-NOV-199 O1-NOV-199 O1-NOV-199 NEURTURIN 1 BETA RELATI GENAPOR GENAPORA OR GI MUS MUSCULLI EUKARYOTA; EUTHERIA;
PRT; 463 AA. EASTED) ST SEQUENCE UPDATE) ST ANNOTATION UPDATE) PRECURSOR (NTUR-ALPHA) (NETUR-ALPHA) PRECURSOR (NTUR-ALPHA) (NETUR-ALPHA) C FACTOR RECEPTOR 2) (GDNF RECEPTOR BE: C FACTOR RECEPTOR 2) (GDNF RECEPTOR BE: L. ZIMONJIC D.B., POPESCU N.C., L., ZIMONJIC D.B., L.	52 357 357 443 443 443 1443 1443	ULAR UTY). SPECI NGLIA NGLIA TIVE A TIVE 1TY: 1TY: LYCOP	ROM N.A. 7325791. , TANSEY ! , TANSEY ! M. JR., M. 793-802(1: 793-802(1: COSPHORYLA. IATE GDNF	(REL. 3) (REL. 3) (REL. 3) (REL. 3) (REL. 3) (RECEPTOR 1) (RED NEUROTI (NOUSE ON 1) (RODENTIA.
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PROPINSKY R.B., CATE R.L
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Q62997;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).
GFRA1 OR GDNFRA OR TENRI OR RETL1.
RATTUS NORVEGICUS (RAT).
TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI PHILLIPS H.S., GODDARD A., MOORE M.W., BUJ-BELLO A., DA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSE
                                                     SEQUENCE FROM N.A. MEDLINE; 96273032.
                                                                                                                               SANICOLA M., HESSION C.A.,
                                                                                                                                               STRAIN-WISTAR;
MEDLINE; 97322:
                                                                                                                                                                    SEQUENCE FROM N.A.
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JING S., WEN D., YU
ANTONIO L., HU Z., C
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TISSUE-RETINA;
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85:1113-1124(1996).
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ROBINSON S., JAWORSKI G., WEI
R.B., CATE R.L.,
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H., TIZARD R., WHITTY
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HU S., ALTROCK
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BETA RELATED NEUROTROPHIC (GDNFR-BETA).

NRTR_HUMAN STANDARD; FALL, O00451; O00451; O1-NOV-1997 (REL. 35, CREATED) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) NEURTURIN RECEPTOR ALPHA PRECURSOR RECEPTOR 2) (GI

GFRA2 OR GDNFRB OR TRNR2.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDA'
EUTHERIA; PRIMATES.
[1]

CHORDATA;

VERTEBRATA;

TETRAPODA;

MAMMALIA

HA) (NRTNR-ALPHA) (TO (GDNF RECEPTOR BETA)

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CHAIN
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1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.

AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.

1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMMITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF REVENEY SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.

1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.

1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U59486; G1399863; EMBL; U97142; G2282022;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                            TPNYVDSS-SLS-VAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTWWQ
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CXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXLPVLMLTXLXXXLXXXLXETS
                      CLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS 468
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430
468 AA;
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llarity 50.7%;
Conservative
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347
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468
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
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Pred. No. 0.00e+00;
12; Mismatches 21:
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GPI-ANCHOR (
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GDNF RECEPTOR
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CRC32;
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MEDILINE; 97325791.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
BALOH R.H., TANSEY M.G., ZIMONJIC D.B., POPESCU N.C.,
HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
JOHNSON E.M. JR., MILBRANDT J.;
NEURON 18:793-802(1997).

10-FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE

TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
GDNR_MOUSE STAI
P97785;
01-NOV-1997 (REL. :
01-NOV-1997 (REL. :
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SEQUENCE
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SUBCELLULAR LOCATION: ATTACHED TO THE MEISTMILARITY).
ALTERNATIVE PRODUCTS: A SHORT FORM IS PR SPLICING IN BOTH BRAIN AND PLACENTA.
SPLICING IN BOTH BRAIN AND PLACENTA.
SIMILARITY: BELONGS TO THE GDNFR FAMILY.
L; APONGATOD; G2145080; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              ---ANKECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYE- 129
                                                                                                                                                                                                                                                                                                                                                                     NYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNVSPKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREI 189
                                                                                                                                                           TELTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLML
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Similarity 53.3%;
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35, CREATED;
35, LAST SE(
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Pred. No. 0.00e+00;
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RECEPTOR
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MISSING (IN SHORT FORM
; 3C74BBFB CRC32;
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Best Local
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GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA
NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; SIGNAL 1 24 POTENT: CHAIN 25 430 GDNF RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO EMBL; AB000800; G1816442; MGD; MGI:1100842; GFRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

11 SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT WITH THE DISPLEIDE-LINKED GDNF DIMER AND WITH 2 (BY SIMILARITY).

11 SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATABE K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA
    435
                                           414
                                                                                    375
                                                                                                                             356
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                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                           E-PVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RERPNCINIQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCILAYSGLIGTVM
                                                                                                                                                                                                                                                                                                                                 LATLYFYLPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSL
  CLSDNDYGKDGLAGASSHITTKSMAAPPSCGLSSLPVMVFTALAALLSVSLAETS
                                                                                  PAPPVQTTTAMTTTAFRIKNKP-LGPAGSENEIP-THVLPPCANLQAQKLKSNVSGSTHL
                                                                                                                                                                 TPNYVDSXXTXXXVAPWCXCRGSGNXXEECEKFLXXFXXNPCLXNAIQAFGNGXDVXMSQ
                                                                                                                                                                                       TPNYIDSS-SLS-VAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQ
                                                                                                                                                                                                                                                                                                                                                                          SMSN-EVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCR--DVACTERRRQTIVPVCSYEE
                                                                                                                                                                                                                                                                                                                                                                                                                   LXTLXSLXXPLXLXXSXXXXXXXXXXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 84.2%;
Similarity 49.7%;
236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369
59
347
406
430
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POTENTIAL.
POTENTIAL.
GPI-ANCHOR
6C64C182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1762; DB 1;
Pred. No. 0.00e+00;
19; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROPHOBIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY A GPI-ANCHOR (12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO FORM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURA'I ION
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    489
                                           468
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SEQUENCE

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Best Local S
Matches 23
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
LIPID
     375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU FOX G.M.;
CELL 85:1113-1124(1996).
-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE AUTOPHOSPHORYLATION AND ACTIVATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                   315
                                                                                                255
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-SUBSTANTIA NIGRA;
MEDLINE; 96270513.
JING S., WEN D., YU Y.,
ANTONIO L., HU Z., CUPPL
                                                                         297
                                                                                                                     238
                                                                                                                                             195
                                                                                                                                                                  181
                                                                                                                                                                                         135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - ! - SIMILARITY: BELONGS TO
                                                                                                                                                                                               122 E-PVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAXITPCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNR_HUMAN
P56159;
                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                          15 LXTLXSLXXPLXLXXSXXXXXXXXXXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXXNXXX 74
                                                                                                                                                                                                                                                                                        3 LATLYFALPILDLLLSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSL 62
SIMILARITY).
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM
WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF
                                                                                         XEXPNCLDLRSXCRTDXLCRSRLADFXTNCXPXXRXXTXCXAXNYXXCLXAYXGLIGTXM
                                                                                                                                                                                                                              XXXXXAXXECXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPY
                     PAPPVQTTTATTTTALRVKNKP-LGPAGSENEIP-THVLPPCANLQAQKLKSNVSGNTHL
                                            TPNYVDSXXTXXXVAPWCXCRGSGNXXEECEKFLXXFXXNPCLXNAIQAFGNGXDVXMSQ
                                                           TPNYIDSS-SLS-VAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGSDYTVWQ
                                                                                                        REKPNCL-LQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGTVM
                                                                                                                                      XXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEX
                                                                                                                                                   SVSN-DVCNRRKCHKALROFFDKVPAKHSYGMLFCSCR--DIACTERRRQTIVPVCSYEE
                                                                                                                                                                                                                                           ASGLEAKDECRSAMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDLLEDSPY 121
                                                                                                                                                                                  601496; -
                                                                                                                                                                                                                                                                                                                             236;
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                       346
405
428
464
                                                                                                                                                                                                                                                                                                                                                                                                                    361
59
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429
                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             368
346
405
                                                                                                                                                                                                                                                                                                                                                                                                                                                     428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JY., HOLST P.L., I
CUPPLES R., LOUIS
                                                                                                                                                                                                                                                                                                                                     81.1%;
49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                         ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                          Score 1696; DB 1;
Pred. No. 0.00e+00;
16; Mismatches 210
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
GPI-ANCHOR
2C8C3574
                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464
                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ⋛
                                                                                                                                                                                                                                                                                                                          210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FANG M., TAMIR
HU S., ALTROCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELATED
                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.₩.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY
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RET (BY
                                                                                                                                                                                                                                                                                                                        Gaps
 434
                                             374
                                                                  354
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                                                                                                                 296
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.8%;
Best Local Similarity 47.1%;
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                               LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSEWIHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
NATURE 387:721-724(1997).

-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO DAEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRTR_CHICK
013157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR BETA)
GFRA2 OR GDNFRB
     377
                              366
                                                        317
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                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA)
                                                                                                              257
                                                                                                                                     246
                                                                                                                                                                 197
                                                                                                                                                                                           188
                                                                                                                                                                                                                   137
                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                             74 ---ANKECQAALEVLQESPLYDCRCKRGMRKEIQCLQVYWSIHLGLAEGEEFYEASFYE- | 2-
                                                                                                                                                                                                                                                                                                                    17 TLXSLXXPLXLXXSXXXXXXXXXXXDCVXAXXXXCXAEXXCSXXYRTLRQCXAGXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                             16 TLRSLAAPPSPPGQDLQGWRVPVDCIRANKLCAAEGSCSSRYRTLRQCLAGRDRNIML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR (BY SIMILARITY).

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR SIMILARITY: BELONGS TO THE GDNFR FAMILY.
                                                                                                                       KPNCLDLRNVCRADHLCRSRLADFHANCQASFQSLTSCPGDNYQACLGSYTGLIGFDMTP
                                                                   NYVDASTTSITISPWCSCKGSGNLEEECEKFLRDFTENPCLRNAIQAFGNGTDVNLSPKN
PSPPITM--LPKVEKSPALPD-DINDSNTMYD-TSIITTCTSIQEHGQKLNKSKEQSLCY 421
                                                  NYVDSXXTXXXVAPWCXCRGSGNXXEECEKFLXXFXXNPCLXNAIQAFGNGXDVXMSQXX 376
                                                                                                     XPNCLDLRSXCRTDXLCRSRLADFXTNCXPXXRXXTXCXAXNYXXCLXAYXGLIGTXMTP
                                                                                                                                                          SXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEXXE
                                                                                                                                                                         SATEHCSRRKCHKALRQFFDNVPSEYTYRLLFCSCK--DQACAEPRRQTIVPFCSYEDKE
                                                                                                                                                                                                              PVTSRLSDIFRXXSXXXXXXXXXXXXXXXSNXCLDAAKACNLNDXCKKLRSAYIXXCXXXX
                                                                                                                                                                                                                              PITSRLSDIFRLASIFSGM--DPATNSKSNHCLDAAKACNLNDNCKRLRSGYISTCSKEL :-
                                                                                                                                                                                                                                                                  XXXAXXECXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPYEX | ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CISNGNYEKEGLGASSHITTK-SMAAPPSCGLSPLLVLVVTALSTLLS--LTETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U90542; G2213805;
                                                                                                                                                                                                                                                                                                                                                                                                                                445
465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         355
387
412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GDNFR-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         355
387
412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                        Score 1607; DB 1; Pred. No. 0.00e+00; 33; M1smatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                               GPI-ANCHOR
5CA073E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEURTURIN RECEPTOR
HYDROPHOBIC, REMOVI
(POTENTIAL).
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CRC32;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA.
GALLING CATTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON ROSENTHAL A., CHINCHERU M., BUCHNAN V.L., DAVIES A.M.; NATURE 387:721-724(1997).

-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPT
                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
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les 212; Conservative
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SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE TWITH THE DISULFIDE-LINKED GDNF DIMER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
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                                                              REKPNCLNLQESCKKNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGTVM
                                                                                                                                                                                                             ATGLEAKDECKSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDLLEDSPY 124
 TPNYVDSXXTXXXVAPWCXCRGSGNXXEECEKFLXXFXXNPCLXNAIQAFGNGXDVXMSQ
                       TPNYIDSS-SLS-VAPWCDCSNSGNDIDECRKFLNFFQDNTCLKNAIQAFGNGTDVNVWQ
                                                                                                XXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEX
                                                                                                                       STSN-EICNKRKCHKALRLFFDKVPPKHSYGMLFCSCR--DVACTERRRQTIVPVCSYED
                                                                                                                                               EXPVTSRLSDIFRXXSXXXXXXXXXXXXXXXXXXXXXIDAAKACNLNDXCKKLRSAYIXXCXX 194
                                                                                                                                                                      E-PVNSRLSDIFRLAPIVSV---EPVLS-KGNNCLDAAKACNLNDTCKRFRSAYITPCTS 179
                                                                                                                                                                                               XXXXXAXXECXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPY 134
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                                                                                                                                                                                                                                                                       LYLALPLADVLLSAEVSGLPGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKESNFSR 65
                                               XEXPNCLDLRSXCRTDXLCRSRLADFXTNCXPXXRXXTXCXAXNYXXCLXAYXGLIGTXM
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Pred. No. 0.
23; Mismatc
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C8D241C9
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POLY-THR.
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Mismatches 219
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CRC32;
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P21783;
01-MAY-1991
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- SUBCELLULAR LOCATION: TYPES I MEMBRANE PROTEIN.

- I- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN

- I- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

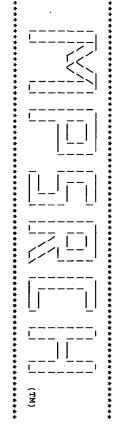
- I- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

- I- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

- I- SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90385285.
COFFMAN C., HARRIS W., KINTN
SCIENCE 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL;
PROSITE; PS00022; EGF 1; 34.
PROSITE; PS01186; EGF 2; 29.
PROSITE; PS01187; EGF_CA; 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
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HSSP; P20693; 1ESL.
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. 34, LAST SEQUENCE UPDATE)
. 36, LAST ANNOTATION UPDATE)
NOTCH PROTEIN HOMOLOG PRECURSOR
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EGF-LIKE 28.
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EGF-LIKE 33.
EGF-LIKE 34.
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EGF-LIKE 34.
EGF-LIKE 36.
3 LIN/NOTCH 1.
EGF-LIKE 34.
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                                                             KRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPYEXP-VTSRLSDIFRXXSXXXXXXXXXXXX
                                                                                              PRG-TQGVHC-EIN-VDDCTPFYDSFTLEPKCFNNGKCIDRVGG-YNCI-CPPGFVGERU
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larity 16.0%;
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Y SIM
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d. No. 9.72e-05;
Mismatches 109;
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Fri Mar 12 13:08:00 1999;

MasPar time 2460.88 Seconds 1236.356 Million cell updates/sec

Tabular output not generated.

Run on:

Description: Perfect Score: >US-08-866-354-41 (1-1699) from US08866354.seq 1699

N.A. Sequence: Comp: 1699

Scoring table: TABLE default Gap 6

Nmatch

STD :

Dbase 0; Query 0

Searched: 2275026 segs, 895388244 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb1-est56
1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
genbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est12 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est52 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est4 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Mean 11.495; Variance 2.154; scale 5.337

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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12	7 10 11	συ4υ δ	Result No.
37	223 128 64 59	349 337 271 254 251	Score 381
2.7	13.1 7.5 3.8 3.5	19.8 14.9 14.9	Query Match
247 478	502 387 252 252	4499 4489 4313	
12 21	112	14 18 21	DB DB
AA754458 W73681	AA238748 W99197 AA754459 AA754459	AA050083 AA925330 AI180186 AA041935 AI179473	ID AA049894
	my35d09.rl Barstead momf59f10.rl Soares mous 97SN1787 Rice Immature 97SN1787 Rice Immature 07SN1784 Pice Immature	mJUBdU5.rl Soares mous UI-R-A1-ek-h-10-0-UI.s EST223927 Normalized r mJ04b08 rl Soares mous EST223187 Normalized r	Description mjlid08.rl Soares mous
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8.83e-05	. 83e-	.82e-	. 40e-	. 82e-	.40e	.40e-	.82e-	.40e-	.82e-	.82e-	.82e-	.82e-	.82e-	.40e-	2.40e-	4.82e-	2.40e-	4.82e-	4.82e-	4.63e-	.10e-	.63e-	.63e-	.10e-	.10e:	.81e-	.81e-	.60e-	.47e-	Ģ	.11e-3

ALIGNMENTS

FEATURES Source	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION
Contact: Maxra M/Mouse EST Project WashU-HMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the MGI:28535 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 405. 1. 442 /organism="Mus musculus"	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Modrant., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. waterston,R. Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996) On Dec 31, 1996 this sequence version replaced gi:1529566.	Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinue; Mus. 1 (bases 1 to 442) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dul:::. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,	AAO49894 91755226 EST. house mouse. Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	AA049894 442 bp mRNA EST 30-DEC-1996 mj11d08.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 475791 5', mRNA sequence.

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BASE COUNT
ORIGIN
                                     SOURCE
ORGANISM
                                                                                                                           DEFINITION
                                                                  KEYWORDS
                                                                                             ACCESSION
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Best Local Similarity 93.6%;
Matches 409; Conservative
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                                                                                       465 bp mRNA mj08d05.rl Soares mouse embryo NDME13.5 clone 475497 5', mRNA sequence.
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                  EST.
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                                                   house mouse.
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/clone="475791"
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142 c
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Pred. No. 0.00e+00;
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AUTHORS
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Best Local Similarity 90.4%;
Matches 424; Conservative
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JOURNAL
                                              239 CTGCACCTCCAGT-TAAGCAGGCCGCTGCCCTTAGAGGAGTCTGCCATGTCTGCAGACTG
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CCTAGAGGCA-CAGAACAACTCAGGAACAGCTCTCTGATAGACTGCAGGTGCCATCGGCG
                             CTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGGAGTCTGCCACATCTGCAGCGTG 31/
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dutrey, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, H., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="embryo"
/dev_stage="13.5-14.5dpc
/lab_host="DH10B"
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/strain="C57BL/6J"
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Pred. No. 0.00e+00;
0; Mismatches 39
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AA925330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track (not shown) served to identify it as a clone from
the normalized adult Kidney library. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 49)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction: two approaches to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: M13 Forward
                                                                         /note*"vector: pyTy3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: The UI-R-Al library is a subtracted library derived from the UI-R-Al library. The UI-R-Al library. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Al) was constructed as follows: PCR amplified cDNA inserts from a pool of approximately 3,840 UI-R-AO clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-AO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806. 1946."
791-806, 1996)"
/db_xref="taxon:10116"
/clone="UI-R-A1-ek-h-10-0-UI"
/clone_llb="UI-R-A1"
                                                                  described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
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1 (bases 1 to 448)
                                                                                                                                                                                                                                                                         Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
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Site_2: NotI"
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                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST project
WashIn-HHMI Mouse EST project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 353)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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AA041935
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Fax: 314 286 1810
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EST.
                                                                                                                      The Institute for Genomic Research 9712, Medical Center Drive, Rockvil Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tlgr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euthori.: Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (Dases 1 to 431)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlayage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                   Contact: Lee, NH
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                                                                                                                                                                                                                                                                                            Rat Genome Project:
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Similarity 88.7%;
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                                               /note="Organ: spleen; Vector:
Site_2: Noti"
/db_xref="taxon:10118"
/clone="RSPCH81"
/clone_lib="Normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /t1ssue_type="embryo"
/dev_stage="13.5-14.5dpc
/lab_host="DH10B"
<1. .>353
                                                                             /organism="Rattus
                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="475095"
/clone_lib="Soares mouse
/sex="unknown"
                                                                                                                                                                                                                                                               (1998)
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114 c
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                                                                                                                                                                                     Drive, Rockville,
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Pred. No. 0.00e+00;
0; Mismatches 36;
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 spleen,
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                                                             pT7T3Pac;
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Soares

Site_1: EcoRI;

(REST) Catalog &

Rat

08-OCT-1998

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Best Local
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l Similarity 99.2%;
252; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryotae; mitochondi
Vertebrata; Eutheria;
                                                                                                                                                                                     MGI:431401
Seq primer
                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
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                                                                                                                                                                                     primer: -28ml3 rev2 ET from Amersham
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                                                                                                                                                                       quality sequence stop: 484.
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9.rl Barstead moo
697841 5', mRNA s
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/organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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JOURNAL
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W99197 387 bp mRNA mf59f10.rl Soares mouse embryo clone 418603 5', mRNA sequence
                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact
IMAGE Consortium (info@image.llnl.gov) for further informatice.
                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 387)

Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone 418603
W99197
                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%;
Similarity 88.3%;
                                                                                                  MGI:253155
                                                                                                                                                                                                                                                                                                                                                                                                              Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nouse mouse
                                                                               primer: ETPrimer
                                                              quality sequence stop:
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/clone="697841"
/clone_lib="Barstead mo/
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="7 day"
/lab_host="DH108"
/organism="Mus musculus"
/strain="C57BL/6J"
                                               Location/Qualifiers
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14.5
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                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
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/note="Vector: pT7T3D-Pac (Pharmacia) with

a modified

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1370 GCACATCCTGTCTGCTCCAGATGAGGTCTTGGAAGAAGCGAGGGCTGTGACCGTTCAGAA 1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCCTAGGACCTTGTAC-TCCAGTTTGGCTGTATATTGTGGTGGTGATTAGCTTCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCTTAGGACTTTGTGGGTCCAGTTTTGCCTTCTGTTCTGATGGTGATTAGCGGCTCAC
Department of Cytogenetics National Inst. of Agri. Sci. & Suwon, Kyunggido, Korea Tel: 82 331 290 0301 Fax: 82 331 290 0307 Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGCCTTCTCCAGGAAGGCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGAGCGGCCAGCTTTCAAACCTC---T---CCTACTTACTCCTG-CTTGGGCTGCTC
                                                                                                                                                                                                                                                                                               92801165
EST.
                                                                                                                                                                                                                                                                                                                            AA754459 252 bp mRNA EST 20-JAN-1998 97SN1187 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
AA754459
                                                                                               Contact: Eun M.Y.
                                                                                                                           Large-scale Sequencing Analysis 
Unpublished (1998)
                                                                                                                             Unpublished
                                                                                                                                                                   1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
                                                                                                                                                                                                                    Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza,
                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                          Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%;
Similarity 82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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/dev_stage="13.5-14.5dpc
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/clone="418603"
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0; Mismatches 37;
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                                                                                                                                                         Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Tel: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science. Myenwith University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji......
Seg primer: M13 Reverse Primer.
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EST.
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P. Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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cDNA clone 97SN1787, mRNA sequence
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National Inst. of Agri. Sci.
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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/organism="Oryza sativa"
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112; Mismatches 77;
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Seq primer: mob.REGA+BT Seq primer: mob.REGA+BT High quality sequence stop: 384. Location/Qualifiers 1. 478 /organism="Homo sapiens" /note="Organ: heart; Vector: pT7T3D (Pharmacia) with. modified polylinker; Site_1: Not I; Site_2: Eco R:: 1:	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL: contact ''. IMAGE Consortium (info@image.lnl.gov) for further information.	The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK WashU-Merck EST Project	```; `` ⊢	g1383826 EST. human. Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	W73681 478 bp mRNA EST 16-OCT-1996 zd55h01.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 374593 5', mRNA sequence.

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Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.G.3,400 expressed sequence tags identify diversity of
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/clone="344593"
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                                                                           mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 0.00e+00;
0; Mismatches 48
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zd55h01.s1
344593 3',
         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordati Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 433)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins; Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marparsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.
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Other_ESTs: THC10206
Contact: Kerlavage,
Bioinformatics
                                                                                                            Homo sapiens
                                                                                                                                                           g1383767
 Trevaskis, E., Waterston, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.0%;
L Similarity 87.2%;
306; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Humindex (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/note="Organ: brain; Vector: lafmid
Site_2: Noti"
/db_xref="ATCC (inhost):150854"
/db_xref="taxon:9606"
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/sex="female"
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Soares fetal heart
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                TGGGGTGGCTGGGAACGAGGGGGCCTT 397,
                                                                                          AAGCTGGTACTGTCACTGAGGTCATCTGGCAAAGAAGGCGTCTTCTCCACCCGAGGGGCC 370
                                                                                                                          TGTTGGCCTTCAGCCCTTGCTCCTGGATAGATGTGCAGGTGGTGATGACACTGG-TCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 650 Std Error: 0.00
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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WashU-Merck EST Project
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/clone="344593"
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Pred. No. 0.00e+00;
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                                                                          TGTTGGCCTTCAGCCCCTGCTCCTGGACAGACGTGCAGGTGGTNATGACACTGGTCCCCA 302
                                                                                                                                                                                    CAGTCAAGGCAGCCGACAGTCTGGCTGTGGAGCCTGAGTTAAGTTTGATCACCTTTT 1972
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GGCTGGTGCTGTCACTGAGGTCATCTGGCAGTGAAGGAGTCTTCTCCACCCGAGGGGCCCT
                                                          TGTTGGCCTTCAGCCCTTGCTCCTGGATAGATGTGCAGGTGGTGATGACACTGGTCCCCA
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WashU-Merck EST Project
Washington University School
4444 Forest Park Parkway, Box
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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310; Conservative
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Eucaryotae; Metazoa; Chordata; Vertebrata;
Eucaryotae; Metazoa; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 358
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact of IMAGE Consortium (info@image.llnl.gov) for further info@mas.
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Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,H.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marid,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,F. al.
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/clone="124377"
92 c 101 g 10
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                                                                                                                                                                                                                                                                                                                                                                         Score 262; DB 5; L4
Pred. No. 0.00e+00;
0; Mismatches 52;
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                                         GCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGCCCAGCGAGTACACCTACC 180
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GCATGCTCTTCTGCCTGCCAAGACCAGGCGTGGGCTGAGCCGGGGGA-AAACCATCC
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                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
High quality sequence stops: 278
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
washIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichth; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 521)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Fax: 314 286 1810
                                                                                                                                                                                                                                     Similarity
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larity 89.3%;
Conservative
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/clone="43207"
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Pred. No. 0.00e+00;
0; Mismatches 32;
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Best Local Similarity 92.18;
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                        ACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGCCCCAGCGAGTACA 180
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Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; continct
IMAGE Consortium (info@image.linl.gov) for further information
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Eutheria; Primates; Catarrhini; Hominidae;
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/clone="124377"
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                                                                                                                                                                     Score 191; DB 5;
Pred. No. 0.00e+00;
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                                                                                                  1 CCACCTGCCACGTCTGTCCAGGAGCAGGGGCTGAAGGCCAACAACTCCAAAGAGTTAAGC
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EST57915
AA350341
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Other_ESTs: EST57914 THC102061
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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                                                                                                                                                                                                                                       Similarity
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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llarity 84.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arkerlav@tigr.org
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Infant brain
                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="infant"
<1. .>416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Infant brain"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="ATCC (inhost):151218"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                            116 c
                                                                                                                                                                                             Score 190; DB 25;
Pred. No. 0.00e+00;
0; Mismatches 41
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REFERENCE
AUTHORS
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                                                                      43
TGTGTGTGTGTGTGTTTCCATTTCGTCAGGCGGCTGTTCTTGTCTTGCGTANTTTTCAA ::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomla; Chordata; Vertebrata; Gnathostomata; Osteic Sarcopterygii; Choanata; Tetrapoda; Amiota; Mammalia; The Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone-43207 library-Soares infant brain lNIB vector-Lafmid BA host-DHIOB (ampicillin resistant) primer-promega -21ml3 Rsitel-Not I Rsite2-Hhd III whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' strand-cDNA was primed with a Not I - oligo(dT) primer [5' AACTGCGAAGAATTTCTTTTTTTTTTTTTTTTTTTTT] ]; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9869171
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                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stops: 364
Source: IMAGE Consortium, LINI
This clone is available royalty-free through LINI;
IMAGE Consortium (info@image.llnl.gov) for further
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University Scho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-Merck EST Project
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                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                               73
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/clone="43207"
94 c 116 g 12
                                                                                                                                                                      8.5%;
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                                                                                                                                      Score 188; DB 16;
Pred. No. 0.00e+00;
0; Mismatches 51
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la; Theria;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                           Department of Pharmacology
University of Colorado Health Sciences Center
Box C256, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
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T03342
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Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Ktevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M.
                                                                                                                                                                                                                                                                                                                                                 Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                     Fax: 3032707097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature Genet. 2, 180-185 (1992)
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                  60
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Infant brain,
                ø
                                                                                                                                                 /note="Vector: BA, Mi3-derived; Site_1: HindII; Site_2: Not!; The infant brain library, constructed by Bento Soares, Columbia University, was oligo-(dT) primed and directionally cloned into an Mi3-derived plasmid using total brain mRNA from a 72-day old human female afflicted with spinal muscular atrophy."

/db_xref="ATCC (inhost):85975"
                                                               /clone_11b="Intant brain, Bento
/lab_host="E. coli DH5-alpha"
complement(<1. .>319)
/gene="DS8551E"
              /gene="D0S8551E"
73 c 87
                                                                                                                                        /clone="IB1289"
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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EST90281
AA377675
                  For clone availability, additional sequence and exinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
                                                                                                                    Email: arkerlav@tigr.org
                                                                                                                                                   Fax: 3018699423
                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
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Eukaryotae; n
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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232; Conservative
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Location/Qualifiers
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he TIGR Human
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Best Local Similarity 85.4%;
Matches 187; Conservative
                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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26
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CANCCGCCGCCTGGACGCCGCCNAAGCCTGCNACATCGACGANACCTGCCAGAAGCTGCG
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                                                                                                                                                                                                                                                                    Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohelp@hgmp.mrc.ac.uk vector: pBluescript II KS V_type: phagemid FRIMER: KS
                               l Similarity
217; Conse
                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 566)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Per
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS; genome survey sequence
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                                                                                                                                                                                                                           sequence.
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                               Conservative
                                                                                                         /organism="Fugu rubripes"
/db_xref="taxon:3103"
/clone_11b="cosmid 142F04"
/clone="142F04aD9"
a 184 c 157 g 74 t
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
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/dev_stage="adult, 20 yrs"
<1. .>225
82 c 59 g 46 t
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="ATCC (inhost):182049"
/db_xref="taxon:9606"
                                                                                                                                                                                                      Location/Qualifiers
                                             66.88;
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GSS
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Pred. No. 1.62e-246;
                            Score 116; DB 27; 1
Pred. No. 2.50e-176;
0; Mismatches 107;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Seisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Derrood, K., Moore, K., Schellenberg, K., Steptoe, M., Tan, F., Derrood, K., Moore, K., Schellenberg, K., Steptoe, M., Tan, F., Derrood, K., Moore, K., M
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Washington University School of MedicineP
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Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
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Best Local Similarity 64.48;
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                                 CDNA
                                                          Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 163)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy ProTumor Gene Index
                                                Email:
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                            l: Robert_Strausberg@nih.gov
Library_Preparation: M. Ben
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/lab_host="DH10B" 51 c 53 (

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                                                                                                                                                                                               /organism="Homo sapiens"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(d primer [5']
Location/Qualifiers
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FEATURES

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TITLE JOURNAL COMMENT REFERENCE AUTHORS RESULT LOCUS SOURCE KEYWORDS ACCESSION DEFINITION ORGANISM COntact: Marra M/Mouse EST project WashU-HHMI Mouse EST project WashIngton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Lo 1 (bases 1 to 446)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubnyke, F., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Hurida; g2040052 EST. vc18b07.rl Ko mouse 5', mRNA sequence. AA387098 The WashU-HHMI Mouse EST Project Unpublished (1996) AA387098 Waterston, R. house mouse. 446 bp embryo mRNA 5dpc Mus musculus cDNA clear 23-APR-1997

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                                                           AAO64450
180 bp mRNA EST ml47hl1.rl Stratagene mouse testis (#937308) Mus clone 515205 5', mRNA sequence.
AAO64450
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:467757
EST.
house mouse
                                             g1558441
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/strain="C57BL/6J"
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/clone="774901"
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Search completed: Fri Mar 12 10:00:36 1999 Job time : 6068 secs.

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., ...
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris ...
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Marris ...
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordana;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Majiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
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                                                                                                                                                                        99;
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Similarity 94.78;
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                                                                                                                                                                                                                                                                                                 /dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
<1. .>180
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Ave, insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                       /sex="males"
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene mouse testis (#937308)"
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0; Mismatches 5;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm MasPar time 6064.12 Seconds 1249.739 Million cell updates/sec

Thu Mar 11 18:15:43 1999;

Tabular output not generated.

Run on:

>US-08-866-354-35 (1-4232) from US08866354.seq 4232

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 CATGAAGAAACCTCAGTAAG......AAGGCTCCAATAAACGTGCG 4232 GTACTTCTTTGGAGTCATTC......TTCCGAGGTTATTTGCACGC

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 segs, 895388244 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb1-est56
1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
genbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 12.815; Variance 2.593; scale 4.942

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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FEATURES Source	TITLE JOURNAL COMMENT	REFERENCE	RESULT 1 LOCUS DEFINITION ACCESSION ACCESSION KEYWORDS SOURCE SOURCE
444 Forest Park Parkway, Box 8501, St. Louis, MO 6310W Tel: 314 286 1810 Email: estewatson.wustl.edu Email: estewatson.wustl.edu IMAGE Consortium (info@image.lln1.gov) for further info	Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK WashU-Merck EST Project WashU-Merck EST Project WashIngton University School of Medicine	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 478) 1 (bases 1 to 478) 1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and	W73681 478 bp mRNA EST 16-OCT-1996 zd55h01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 5', mRNA sequence. W73681 g1383826 EST. homon sapiens

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Primates; Catarrhini; Hominidae; Homo.

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Pred. No. 0.00e+00;
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W73633 433 bp mRNA zd55h01.sl Soares fetal heart 344593 3', mRNA sequence.

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Best Local Similarity 97.3%;
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   CCCCAAAGGGAGGCCTGCCAA
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                                                                  AAGCTTGAGGGCCCACGGTGCTGCAGACACACCCCGGCTGTGGTCTCTCCCCTCCTCT
                                                                                  AAGCTTGAGGGCCCA-GGTGCTGCAGACACACCCCGGCTGTGGTCTCTCTCCCCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
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/note="Vector: pAMP10; mRNA made from Ewing's surce:
/note="Vector: pAMP10; mRNA made from Ewing's surce:
cDNA made by oligo-dT priming. Non-directionalize:
Size-selected on agarose gel, average insert size
Size-selected on agarose gel, average insert size
Reference: Krizman et al. (1996) Cancer Research
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/clone=lib="NCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
104 c 119 g 121 t
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56:5380-5383."
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EST.
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WashU-Merck EST Project
WashIngton University School of Medicine
WashIngton Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 433)
1 (bases 1 to 433)
1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Unpublished (1995)
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llarity 97.9%;
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/lab_host="DH10B (ampicillin
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109 c 132 g 120 t
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/clone="344593"
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EST57915
AA350341
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Initial assessment of human gene diversity and expression parameters.
                                                                                                                                                                                                                                                                                                                                                                                                Seq
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and ex
information related to this EST, please check the
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Tel: 3018699056
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Other_ESTs: EST57914 THC102061
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Site_2: Noti"
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Infant brain
                                                                                                                   /clone_lib="Infant brain"
/sex="female"
                                                                                /dev_stage="infant"
                                                                                                                                                                             /db_xref="ATCC (inhost):151218"
/db_xref="taxon:9606"
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'note="Organ: brain; Vector: lafmid
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Query Match

8.48;

Score 357;

8

25;

Length 416;

Local

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RESULT 5
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1 (bases 1 to 364)

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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                  Email: est@watson.wustl.edu
High quality sequence stops: 358
High quality sequence stops: 358
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project 
Unpublished (1995)
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390; Conservative
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Fax: 314 286 1810
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Cloning_method:
  cloned 5' -> 3'
  vector;
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Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry J. J. and Genetique Moleculaire et Biologie du developpement B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress that 2 (bases 1 to 353)
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EST; partial cDNA sequence;
                                                                                                                                IMAGE: molecular integration of the analysis
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/clone="124377"
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                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 432)
Berry.R., Stevens,T.J., Walter,N.A.R., Wilcox,A.S., Rubano,T., Hopkins,J.A., Weber,J., Goold.R., Soares,M.B. and Sikela,J.M. Gene-based Sequence Tagged Sites (STSs) as the basis for a human
                                                                                                                                                                                                                                                                                      sequence.
T15637
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Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
                                                                                                                                                                                                                   Homo sapiens
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/db_xref="taxon:9606"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
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Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
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/db_xref="ATCC
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(inhost):85998" (inhost):85999"

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Best Local Similarity 96.7%;
Matches 408; Conservative
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Pred. No. 0.00e+00;
0; Mismatches 4
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CAGCTTGGGGACCAGTGTCATCACCACCTGCACGTTTNTCCAGGAGCAGGGGCTGAAGGC
                                                                                                                       CACCCAGGCCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTAC
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EST56965
AA349976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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Adams, M.D., Kerlavage, A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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larity 96.0%;
Conservative
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/note="Organ: brain; Vect
Site_2: NotI"
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/db_xref="taxon:9606"
/clone_lib="Infant brain"
/sex="female"
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Pred. No. 0.00e+00;
0; Mismatches 13
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                            GCTCTGTGAAGCACATGCTTAACTCTTTGGAGTTNTTGGCCTTCAGCCCCTGCTCCTGGG 310
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ACAGAACGTGCAGGNTGGGTGATGACACTGGGNCCCCAAGGCTGGGTACTGTCACTGAGG
                                                                                             IGCTGGGGCCTGAGTTAGGTTTGATCACCTTGTTACTCCCTGGGATGATATTTGTCGTGA 2x...
                                                                                                                                                             ACAAGGCCAGTTTCAGCATCAGGACAGACAGCACGGTCAAGGCAGCCGACGGTCT(\circ)\circ
                                                                                                                                                                                                                                                                                          Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Osteichth: Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichth: Sarcopterygil; Choanata; Tetrapoda; Anniota; Mammalia; Theria Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Wohldmann,P. and
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y170a10.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact
IMAGE Consortium (info@image.llnl.gov) for further inter-a-
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Unpublished (1995)
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WashU·Merck EST Project
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Similarity 95.1%;
388; Conservative
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                                          CGAGGCATTAAAACTTGGGCACCAGCTTCTTTNTCGGTGGCAGAAATTTTNAAGTCAGAG 120
                                                                                       GGCTGGGGGCCAGCTCCAGGAGGGGCTTGAGAGCTCAGCCTGCGTGGGAGAGCCCCTTGTGG 3687
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                                                                                                                                                                                                                                                                                                                                                                                              Stretch_removed: nothing
Normalization_method: Bento Soares,
Genexpress_library_idt: C;
Genexpress_sequence_idt: y1c-zya05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cloning_method:
  cloned 5' -> 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A. Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 317)
Auffray, C., Behar, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Genexpress cDNA program Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer: M13_reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; partial cDNA sequence; transcribed sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequence colinear to mRNA
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larity 96.8%;
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                                                                                                                                                                                                                                                                        /clone_lib="normalized infant brain cDNA Psychiatry Dept. Columbia University USA" /sex="female"
                                                                                                                                                                                                                          /tissue_type="total brain"
/dev_stage="3 months old"
84 c 87 g 89 t
                                                                                                                                                                                                                                                                                                                        /isolate="muscular atrophy patient"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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to 317)
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   CAACCATTGCCTGG-ATGCTGCCAAGGCCTGCAACCTGAATGACAACTGCAAGAAGCTGC :: : : -
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Hillar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hillar,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marre,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. wird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Eukaryotae; Metazoa; Eumetazoa; Gnathostomata; Osteichthyos: Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyos: Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLN
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WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB: G00-415-748
                                                                                                                       h 7.3%;
Similarity 93.6%;
396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for for the construction of the constructi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/clone="43207"
154 c 144 g 119
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                                                                                                                    Score 307; DB 16;
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                                                                                                                                                                                             Fax: 301869423
Email: arkerlav@tigr.org
Emoil: arkerlav@tigr.org
For clone availability, additional sequence and ex
information related to this EST, please check the
Index (http://www.tigr.org/tdb/hgi/hgi.html).
Location/Qualifiers
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Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.C.
3,400 expressed sequence tags identify diversity of transcripts
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/note="Organ: brain; Vector: lafmid Site_2: NotI"
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                                                                                              /db_xref="ATCC (inhost):151218"
/db_xref="taxon:9606"
/clone_11b="Infant brain"
/sex="female"
                                                                                 /dev_stage="infant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex Franciand Genetique Moleculaire et Biologie du developpement, CNRS UPR4-0 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.ir 2 (bases 1 to 309)
No significant homology found with
                                                                     CDNA sequence colinear to mRNA Stretch_removed: nothing Normalization_method: Bento Soares, Genexpress_library_idt: C:
                                                                                                                                                                              Sequencing_method: single read,
Primer: M13_reverse
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                                                                                                                  Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C336, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
                                                                                                                                                                                                      On Jul 31, 1993 this sequence version
                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 319)
Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M.
Single pass sequencing and physical and genetic mapping of human
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IB1289
                                                        Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
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llarity 97.7%;
Conservative
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9 Infant brain, 1
, mRNA sequence.
/organism="Homo sapiens"
/note="Vector: BA, M13-derived; Site_1: HindIII; Site_2:
NotI; The infant brain library, constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
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/db_xref="taxon:9606"
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1 (Dases 1 to 359)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 6.8%;
l Similarity 94.7%;
303; Conservative
           The WashU-Merck EST 
Unpublished (1995)
                                                                                                                                                         Homo sapiens
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/lab_host="E. coli DH5-alpha"
complement(<1. .>319)
/gene="DOS8551E"
<1. .>319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directionally cloned into an M13-derived plasmid using total brain mRNA from a 72-day old human female afflict with spinal muscular atrophy. "
/db_xref="ATCC (inhost):85975"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soares, Columbia University, was oligo-(dT) primed and directionally cloned into an M13-derived plasmid using
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Pred. No. 0.00e+00;
0; Mismatches 16
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                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 312
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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/clone="123205"
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signal transduction; human: 1; renal failure; nephritis; 1ypoxic injury; 1isease; multiple sclerosis; 1creutzfeldt-Jakob disease; 1njury; Down's syndrome; 1ular dystrophy; 1; ss. 1ss. 1ss. 1ss. 1ss. 1ss. 1ss. 1ss.	(dC-dA)n.(dG-dT)n pol 5 Repeat sequence from 6 Repeat sequence from 7 Repeat sequence from 6 Repeat sequence from 6 Repeat sequence from 7 Repeat sequence from 6 Repeat sequence from 6 Repeat sequence from 7 Repeat sequence from 9 Repolymorphic repeat se 9 Fragile x diagnostic 7 Polymorphic repeat se 9 Fragile x diagnostic 8 Fragile x diagnostic 9 Polymorphic repeat se 9 Reman RADCCOMPB CDNA 9 Ruman RADCCOMPB CDNA 9 Ruman RADCCOMPB CDNA 9 Ruman RADCCOMPB CDNA 9 Ruman RADCCOMPB CDNA 9 ROUSE lactoferrin gen 9 Ruman RADCCOMPB CDNA 9 ROUSE lactoferrin gen 9 ROUSE lactoferrin gen 9 ROUSE lactoferrin gen 9 ROUSE lactoferrin 7 Retroviral recumulatin 3 Retroviral vector MFG 1 PAS 741 insert contg. 1 Retroviral vector pAdDel 1 POLYMORPHIC repeat se 8 Base substituted E.co 6 Rat cryptdin 3 gene. 6 Rouse SRY-related gen 6

밁 Š В Ş ş 밁 8 ₽ Ş 밁 Ş 밁 Ş 밁 δô 밁 õ 밁 ş 밁 Ş 용 ş 밁 9999999999999999999 CC RetL1 (see W37457). Rat and human retL1, and mouse and human retL3 CC DNA sequences are also claimed (see v00245-47 and v00249-51).
CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host CC vectors containing retL2 plan and prokaryotic or eukaryotic host CC cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL2, its soluble variants and CC fusion proteins with a toxin, imageable compound or radionuclide. RetL2, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, see in renal failure, nephritis, kidney transplants, toxic or hypoxic constraints and cc injury, neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy constraints or prion infections (e.g. meningitis, myelopathy cand cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis). Cc system (Lyme disease, muscular dystrophy and myasthenia gravis). Sequence 1888 BP; 399 A; 593 C; 536 G; 360 T; Query Match
Best Local Similarity
Matches 1886; Conser 2223 1743 1683 1 BABABACGGTGGGATTTATTTAACATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCTTT 1622 2163 2103 2043 1923 1803 1623 1983 1863 481 421 361 301 181 121 721 241 61 cacctggggctgaccgagggtgaggagttctacgaagcctccccctatgagccggtgacc ctggccaacaaggagtgccaggcggccttggaggtcttgcaggagagcccgctgtacgac cgccggcaaaccatcctgcccagctgctcctatgaggacaaggagaagcccaactgcctg agcgagtacacctaccgcatgctcttctgctcctgccaagaccaggcgtgcgctgagcgc gagcgctgcaaccgccgcaagtgccacaaggccctgcgccagttcttcgaccgggtgccc aactgcaagaagctgcgctcctcctacatctccatctgcaaccgcgagatctcgcccacc 9t99tcagcgccaagagcaaccattgcctggatgctgccaaggcctgcaacctgaatgac tcccgcctctcggacatcttcaggcttgcttcaatcttctcaggggacagggcagacccg tgccgctgcaagcggggcatgaagaaggaagctgcagtgtctgcagatctactggagcatc tgcagctctcgctaccgcactctgcggcagtgcctggcaggccgcgcgaccgcaacaccatg ggctggcgcccccagtggactgtgtccggggccaatgagctgtgtgccgccgaatccaac 180 CTAGACGACACCCTCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCCCCGAGCTCCAC 1682 GAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGCCC GTGGTCAGCGCCAAGAGCCAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATGAC TCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACCCG TGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCTGGCAGGCCGCGACCGCAACACCATG GGCTGGCGCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCCGCCGAATCCAAC AGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGCGC AACTGCAAGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCACC 44.5%; ilarity 99.9%; Conservative Score 1884; DB 39; Length 1888; Pred. No. 0.00e+00; 0; Mismatches 2; Indels 0; 0 Gaps 660 420 300 780 2282 720 2222 600 2102 540 480 1982 1922 360 1862 240 1742 2162 2042 0

•	ACCGGACAAGAGCCTGCAGCGGAAGGGACTCTGGGCTGCCTGAGGCTGGCT		0y 5
	CTAGAAATGCCCTTCACTTTCTCTGGTGTTTTTCTCTCTGGACCCTTCTCTAA.3;	17/1	; S
•	totagaaatgcccttcactttctcctggtgttttttctctctggacccttctqqqqcqqqqqqqqqq	68	말
	GAGAGCTGGCCCAGGGGTCCCCTGGCAGGGGAAACTCTGGTGCCGGGGAGGGGCACACTAGAACACAGGGGAAACTCTGGTGCCGGGGAGGGCCACACTAGAACACAGGGGAAACTCTGGTGCCGGGAAGGGCCACACTAGAACAACAGGGGAAACTCTGGTGCCGGGGAAGGCCCACACTAGAACAACAAGAACAAGAACAAGAAGAAGAAGAAGAAGAA	3183	Qy
ē -	agagotggocoaggggtococotggoaggggaaactotggtgooggggaaaaaanaa	1621	문
	CCCAGGTTTCTCTCGGAGAAGTTTTGTAAACCAAACAGACAAGCAGGCAG	3123	δ δ
	CACACACCTTGCAAAAAAAATTGTTTTTCCCACCTTGTCGCTGAACCTG	n C	; S
in F	acacacacaccttgcaaaaaaaaattgtttttcccaccttgtcgctgaacctgtct.ccl	50	}
?	TTTTGAAAGCTACGCAGACAAGAACAGCCGCCTGACGAAATGGAAACACACAC	3003	Qy
180	atttttgaaagctacgcagacaagaacagccgcctgacgaaatggaaacacacac	1441	В
3002	ACCGTGCTGTCTGTCCTGATGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAGAA	2943	Qy
1440 .	ccgtgctgtctgtcctgatgctgaaactggccttgtaggctgtgggaaccgagtcagaa	1381	망
2942		2883	Qy
1380	gtaacaaggtgatcaaacctaactcaggccccagcagagccagaccgtcggctgccttg	1321	함
2882	AACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAATATCATCCCAGGG	2823	Qy
1320	caactccaaagagttaagcatgtgcttcacagagctcacgacaaatatcatcccaggg	1261	망
2822	AGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGGCC	2763	Qy
1260	gcttggggaccagtgtcatcaccacctgcacgtctgtccaggagcaggggctgaaggcc	1201	d D
2762	ACCCAGGCCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTACC	2703	Qy
1200	cccaggcccctcgggtggagaagacgccttctttgccagatgacctcagtgacagtacc	1141	₽
2702	CAGGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCAAAAGGCCCCTCGTTCCAGGCC	2643	Qy
1140	aggcctttggcaacggcacggacgtgaacgtgtccccaaaaggcccctcgttccaggcc	1081	₽
2642	GAGGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCCATGCCTCCGGAACGCCATC	2583	Qy
1080	aggagtgtgagaagttcctcagggaacttcaccgagaaccccatgcctccggaacgccatc	1021	Дb
2582	AGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGGAG	2523	Qy
1020	gccccactggcatcgtggtgtccccctggtgcagctgtcgtggcagcgggaacatggag	961	ф
2522	TGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACTCC	2463	Qy
(ièi)	gtctgggctcttatgctggcatgattgggtttgacatgacacctaactatgtggactcc	901	Ъ
t. L	GCCAATTGTCGAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGGCG	2403	Qy
-	ccaattgtcgagcctcctaccagacggtcaccagctgccctgcggacaattaccaggc	841	В
•	GACCTGCGTGGCGTGTGCCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGAC(11 C.) A.	2343	Qy
ż	acctgcgtggcgtgtgccggactgaccacctgtgtcggtcccggctggccgactlo	781	ర్జ
•		2283	Qy

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                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                           2179
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Human EST-derived sequence yI70al0.rl.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy;
expressed sequence tag; EST; ss.
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Klein RD, Moore MW, Rosenthal A,
WPI: 97-470819/43
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                                                                        2239
                                                                                                                                                                                                                  2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders, particularly enteric nervous system or kidney disorders, particularly enteric nervous system or kidney disorders, page 61; 10pp; English.
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WO9733912-A2.
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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                                                                                                          181
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                                     241
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tgcccagctgctcctatgaggacaaggagaagcccaactgcctggacctgcgtggcgtgt 300
                                                                                       gcatgctcttctgctcctgccaagaccaggcgtgcgctgagcgcgcggggcaaaaccatcc
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                                                                                                                                           GCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGCCCAGCGAGTACACCTACC
                                                                                                                                                                                                                GCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCACCGAGCGCTGCAACCGCC
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                                                                      GCATGCTCTTCTGCCTGCCAAGACCAGGCGTGCGCTGAGCGCCGGCCAAACCATCC
                                                                                                                                                                                                                                                                                                                                                          8.5%;
llarity 95.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 knockout animals are also claimed. BP; 86 A; 152 C; 121 G;
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Pred. No. 3.82e-219;
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                                                                                                                                                                                                            PT Isolated gilial cell derived neurotrophic factor receptor alpha - PT Isolated gilial cell derived neurotrophic factor receptor alpha - PT disorders, particularly enteric nervous system or kidney disorders probable is page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence derived sequences, including human come factor receptor (GDNFR) sequences, including human come designated y170alo. If (see T84979), and come fragments of these EST-derived sequences (see T84989-81) or compression of the factor receptor. In particular, it relates to novel use of come fails and its receptor. In particular, it relates to novel use of come fails and its receptor. In particular, it relates to novel use of some fails and to the GDNFR alpha, including agonist and neutralising come fails of the GDNFR alpha, including agonist and neutralising compression of the the GDNFR alpha, including agonist and neutralising compression of the physiological role of GDNFR alpha, including sponist and collective for identifying molecules homologous to GDNFR alpha, alpha, and claimed conditions, particularly kidney disease associated with conditions, particularly kidney disease associated with conditions and knockout animals are also claimed.

Sequence 351 BP; 77 A; 117 C; 96 G; 57 T;
                                                                                                                                              Query Match
Best Local S
Matches 30
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T84978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human EST-derived sequence ye83h05.rl. Glial cell derived neurotrophic factor receptor alpha; GRANGE GDNF; human; kidney disease; glomerulonephritis; therapy; Time GDNF; human; kidney disease; glomerulonephritis; therapy;
     2112
                                                                     39 gccaagagcaaccattgcctggatgctgccaaggcctgcaacctgaatgacaactgcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
Klein RD, Moore MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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WO9733912-A2.
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Bagetgegetcetectacatetecatetgeaacegegagatetegeceacegagegetge 158
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                                                                                                                                                Similarity
302; Conser
                                                                                                                                              7.0%;
larity 96.5%;
Conservative
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                                                                                                                                          Score 295; DB 37; Le
Pred. No. 4.75e-175;
Pred. "---+ches 11;
                                                                                                                                                                              Length 351;
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                                                                         PT Glial cell line derived neurotrophic factor receptor - useful to pr treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease
PS Claim 17; Pages 96-98; 196pp; English.
CC The present sequence encodes the rat glial cell line-derived concurred for nerve cell disorders, e.g. Parkinson's and Alzheimer's dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's CC disease or amystrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) CC and Huntington's disease and (optionally in combination with GDNF) CC disease or amystrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) CC disease or amystrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in cased by injury to combine the seary neurons. The receptor can also be used to block CC unwanted GDNF in pharmaceutical formulations. Receptor expressing CC cells, preferably transfected ex vivo, can be used to dientify by injury to implantation, and the use of the receptor CDNA in gene therapy is called the sease of the conditions and the sease to identify combined to contemplated. Probes based on the CDNA can be used to identify who combined the complex with the condition of GDNF therapy, and abnormalities in receptor can be used to monologous/cross reactive with the cDNA and animal combined to detect GDNF dependent neurons or processes and the antibody combined to detect GDNF dependent neurons or processes and the antibody combined the combined transduction by GDNF, i.e. complex that mediates/enhances signal transduction by GDNF, i.e. complex that mediates and the antibody complex that mediates/enhances signal transduction by GDNF, i.e. complex that mediates and the combined c
  Query Match
Best Local S
Matches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2352
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Fox GM, Jing S, Wen D;
WPI; 97-535836/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1997; U06281.
14-APR-1997; US-837199.
22-APR-1996; US-015907.
09-MAY-1996; US-017221.
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T95297;
01-MAY-1998 (first entry)
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30-OCT-1997.
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    Local Similarity
les 592; Conse
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5.3%;
larity 65.7%;
Conservative
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Score 223; DB 38;
Pred. No. 7.51e-126;
0; Mismatches 297;
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                                         Length 2138
    Indels
Gaps
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502 ggccaaggatgagtgccgtagcgccatggaggccttgaagcagaagtctctgtacaactg

561

V00245 standard; cDNA;

48

21-MAY-1998 (first entry)
Rat Ret ligand retLl cDNA.
Ret ligand; RetL; RetLl; receptor; signal transduction; rat;
cell growth; renal cell; nerve cell; renal failure; nephritis;
kidney transplant; toxic injury; hypoxic injury;
neurodegeneration; motor neurone disease; multiple sclerosis;

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CC that codes for the Ret ligand RetLl (see W37457), a key component
CC of the Ret signalling pathway. It consists of the insert of clone
CC #230-5A-86-17 that was isolated from a rat embryonic kidney cDNA
CC expression library using a rat Ret/IgG fusion protein. The
CC isolated cDNA was used as a probe to identify human retLl CDNA
CC (see V00246-47). retL2 and retL3 cDNAs have also been identified
CC (see V00248-51). vectors containing retL1 DNA and prokaryotic or
CC enkaryotic host cells transformed or transfected with these vectors
CC soluble variants and fusion proteins with a toxin, imageable
CC compound or radionuclide. RetL1, optionally when expressed from
CC vectors in vivo, is used to promote growth of new tissue and
CC survival of damaged tissue, particularly kidney or neural tissue.
CC Typical applications are in renal failure, nephritis, kidney
CC confoints, toxic or hypoxic injury, neurodegeneration, motor
CC infections (e.g. meningitis, myelopathy associated with HIV or
CC reutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC or conditions involving the peripheral nervous system (Lyme
CC disease, muscular dystrophy and myasthenia gravis). Fusion
CC especially tumours.
SO Sequence 3616 BP: 876 A: 955 C: 921 G: 864 T.
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Best Local :
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27-NOV-1997: U07726.
10-AAR-1997: US-017427.
10-AAR-1996: US-017427.
07-JUN-1996: US-01859.
16-JUL-1996: US-021859.
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel M WPI; 98-018431/02.
P-PSDB: W37457.
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Claim 1; Page 46-49; 113pp;
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Pred. No. 7.51e-126;
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27-APR-1998
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27-APR-1998 (first entry)
Rat glial cell derived neurotrophic factor receptor alpha
Glial cell derived neurotrophic factor receptor alpha; (CD)
CONNET rat: kidney disease; glomerulonephritis; therapy: (3)
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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(GETH) GENENTECH INC. Klein RD, Moore MW, Rosenthal WPI; 97-470819/43.

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PT isolated gilal cell derived neurotrophic factor receptor alpha seful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders products, particularly enteric nervous system or kidney disorders products, particularly enteric nervous system or kidney disorders produced for full-length rat gilal cell derived neurotrophic call factor receptor alpha (GDNFR alpha) (see W27327), a novel creceptor receptor system for GDNF. It was isolated by expression cloning. CC receptor system for GDNF. It was isolated by expression cloning. CC clones were transfected in a cytomegalovirus-based vector. cDNA clones were transfected into COS 7 cells and expression of cultative GDNF receptors was detected by binding of iodinated GDNF. CC a single positive pool was obtained, from which the cDNA clone was collated. An expression vector containing the cDNA clone was collated. An expression vector containing the cDNA clone was collated to native rat GDNF and its receptor. In particular, it crelates to novel uses of GDNF and its receptor. In particular, it crelates to native rat GDNF and its receptor. In particular, it crelates to native rat GDNF and its various uses for these and neutralising antibodies, as well as various uses for these collars. It also relates to assay systems for detecting ligands ct of GDNFR alpha, systems for studying the physiological role of CDNFR, diagnostic techniques for identifying gDNF-related conditions, methods for identifying molecules homologous to GDNFR alpha, and ct therapeutic techniques (claimed) for the treatment of GDNF-related conditions, particularly kidney disease collarined claimed disorders. Transgenic and knockout animals are also crisined.
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The present sequence encodes the human glial cell line-derived CC neurotrophic factor (GDNF) receptor, which can be used to treut CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's CC disease or amyotrophic lateral sclerosis, complications of dicherence and Huntington's disease and (optionally in combination with GDNF) CC and Huntington's disease and (optionally in combination with GDNF) CC diner ear sensory neurons. The receptor can also be used to highly compared GDNF activity, analyse GDNF related molecules and containing the pharmaceutical formulations. Receptor expression: CC cells, preferably transfected ex vivo, can be used similarly contained GDNF the use of the receptor CDNA in gene there, and contemplated. Probes based on the CDNA can be used to identify contained cells and tissues, e.g. to identify pathers and complex with the collabored transfected molecules that form a complex with the collabored transfected contained that form a complex with the collaboration, and to isolate molecules that form a complex with the collaboration and to isolate molecules that form a complex with the collaboration.
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Claim 17; Pages 91-93; 196pp; English.
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Fox GM, Jing S, Wen D;
WPI; 97-535836/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human glial cell line-derived neurotrophic factor receptor cDNA. Human; glial cell line-derived neurotrophic factor; GDNF; receptor treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glaucoma; retinal degeneration; hearing los; gene therapy; ss.
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T84981 standard; DNA; 201 I
T84981;
27-APR-1998. (first entry)
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Klein RD, Moore MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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W09733912-A2.
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l Similarity 100.0%;
201; Conservative
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Pred. No. 6.05e-111;
0; Mismatches 0;
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Human EST-derived sequence y170al0.rl fragment. Glial cell derived neurotrophic factor receptor

receptor alpha;

GDNFR

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D V00246;
C V00246;
C V00246;
C V00246;
DT 21-MAY-1998 (first entry)
DE Human Ret ligand retL1 partial cDNA.

KW Ret ligand; RetL2; receptor; signal transduction; human;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplant; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Takob disease;

KW cranlal nerve injury; spinal cord injury; Down's syndrome;

KW cranlal nerve injury; spinal cord injury; Down's syndrome;

KW cerebral palsy; Lyme disease; muscular dystrophy;

KW myasthenia gravis; tumour; therapy; ss.
PN SE SULT IRESULT IRE
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CC This DNA sequence comprises a fragment of a human EST-derived concern to the chentify glial cell derived neurotrophic factor receptor (GDNFR) sequences, including human variants. The invention relates to novel uses of GDNF and its receptor. In particular, it relates to novel uses of GDNF and its receptor. In particular, it relates to to rat GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, and creatifying gDNF-related conditions, methods for the physiological role of GDNF, diagnostic techniques for identifying gDNF-related conditions, methods for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with GLONFR alpha and enteric nervous system related disorders.

CC Transgenic and knockout animals are also claimed.

Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
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Best Local S
Matches 20
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Klein RD, Moore MW, Rosenthal A, Ryan AM.
WPI: 97-470819/43.
W09744356-A2
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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Similarity 100.0%;
201; Conservative
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Pred. No. 6.05e-111;
0; Mismatches 0;
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Best Loc Matches

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cctactcggggcttattggcacagtcatgacccccaactacatagactccagtagc-ct-

agccagagtcaaggtctgtcagcagctgtctaaagggaaaactacgctgactgcctcctcg GCGTGTGCCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGACTTCCATGCCAATTGTC CCATCCTGCCCAGCTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCU: ccatcgtgcctgtgtgctcctatgaagaggaggagaagcccaactgtttgaatttgca.vv CCTACCGCATGCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGCGCCGCCGCCAAA gctacggaatgctcttctgctcctgccgggacatcgcctgcacagagcggaaqccaacana v.

GAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGGCGTGTCTGGGCCT

2472

2412

2293

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2233

266

2173

accgccgcaagtgccacaaggccctccggcagttctttgacaaggtcccuqccuqurun;

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Mismatches

219;

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agtacaggtcggcgtacatcaccccgtgca-ccaccagcg-t-gtccaacgatgtcl.gca CCAAGAGCAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATGACAACTGCAAGA

AGCTGCGCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCCACCGAGCGCTGCA

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CC This sequence comprises a partial cDNA for human Ret ligand (RetL) (RetL) (see W37458), a key component of the Ret signalling pathway. CC It was isolated from a human embryonic kidney cDNA library using CC v1 v247) for human retL1 cDNA as probe. A full-length sequence (see CV00247) for human retL1 cDNA has also been obtained, as well as containing retL1 DNA and prokaryotic or eukaryotic host cells containing retL1 DNA and prokaryotic or eukaryotic host cells cas a method for production of RetL1, its soluble variants and considering from vectors in vivo, is used to proteins with a toxin, imageable compound or radionuclide. CC RetL1, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, conjury, neurodegeneration, motor neurone disease, multiple conjury, neurodegeneration, motor neurone disease, multiple conjury, neurodegeneration, motor neurone disease, multiple conjunctions (e.g. meningitis conjunctions end cerebral palsy, or conditions involved (e.g. meningitis conjunctions end cerebral palsy, or conditions involved (e.g. meningitis conjunctions end cerebral palsy, or conditions end (e.g. meningitis conjunctions end (e.g. meningitis 
                                                         Query Match
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07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel
WPI: 98-018431/02.
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07-MAY-1997;
10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nerve cells
Claim 1; Page 58-60; ll3pp; English
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                                    Local Similarity
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US-017427.
US-017427.
US-019300.
US-021859.
3.8%;
llarity 65.6%;
Conservative
                                 Score 161; DB 39;
Pred. No. 4.53e-84;
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This sequence comprises CDNA coding for human Ret ligand (RetL)
RetLl (see W37459), a key component of the Ret signalling pathway.
It was deduced from 2 clones isolated from human foetal kidney
CDNA using primers based on a partial human retL1 cDNA (see
V0246). Rat retL1 and mouse and human retL2 and retL3 sequences
have also been identified (see V00245 and V00248-51). The human
CC retL1 cDNA is 88.2% identical to rat retL1 cDNA. Vectors
CC containing retL1 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
as a method for production of RetL1, its soluble variants and
CC RetL1, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, mephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC peripheral nervous system (Lyme disease, muscular dystrophy and
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
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Ret ligand; RetLi; RetCli; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                nerve cells
Claim 1; Page 62-64; 113pp;
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07-MAY-1997
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WO9733912-A2.

Glial cell derived neurotrophic fa GDNF; mouse; kidney disease; glome. Mus musculus. 27-APR-1998 (first entry)
Mouse GDNFR alpha clone 26 3'
Glial cell derived neurotroph

glomerulonephritis; therapy: se.

T 12 T84977

standard; cDNA;

840

T84977

(GETH) GENENTECH INC. Klein RD, Moore MW, Rosenthal A, WPI; 97-470819/43.

Ryan

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18-SEP-1997. 13-MAR-1997; U04363. 14-MAR-1996; US-618236. 14-MAR-1996; US-615902.

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CC This cDNA sequence comprises the 3' end of mouse full-length color 26; the 5' end of the clone is given in cc gital cell derived neurotrophic factor receptor alpha (GDNFR alpha) cc (see W27327) clone 26; the 5' end of the clone is given in cc rat GDNFR alpha cDNA (see T84975) as probe. The invention relates cr to novel uses of GDNF and its receptor. In particular, it relates cc to notive rat GDNFR alpha (see W27327), its variants and soluble cc derivatives (extracellular domain), chimeric GDNFR alpha and cc antibodies which bind to the GDNFR alpha, including agonist and cc derivatives (extracellular domain), chimeric GDNFR alpha and cc molecules. It also relates to assay systems for detecting ligands cc domains in the physiological role of colors to diagnostic techniques for studying the physiological role of GDNFR alpha, systems for identifying molecules homologous to GDNFR alpha, and cc therapeutic techniques (claimed) for the treatment of GDNF related conditions, particularly kidney disease cc associated with glomerulonephritis and enteric nervous system cc claimed.

CC claimed.
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Matches
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Rat Syntaxin 1B gene.
Binding domain; rat; syntaxin; synaptosomal-associated protein; neurotransmitter; presynaptic membrane; central nervous system;
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27-APR-1998
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larity 64.2%;
Conservative
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10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1989; US-754351.
05-SEP-1991; US-752377.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Example 8; Column 57-58; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequence having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect the repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic discussions commercial animal or plant breeding or pedigree analysis.

The repeats, when analysed, fall into 4 categories:
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(dC-GA)n.(dC-dT)n polymorphic repeat sequence #9.
(dC-M)n.(dC-dT)n polymorphic repeat sequence; genetic marker; primer; ampli-
Polymorphism; repeat sequence; genetic marker; primer; human;
PCR; polymerase chain reaction; paternity; maternity; human;
linkage analysis; genetic disease; animal; plant; breeding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T66072
T66072;
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Scheller RH;
WPI; 98-031743/03.
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larity 84.0%;
Conservative
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Pred. No. 2.73e-13;
0; Mismatches 12
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Matches
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Best Local Similarity 91.8%;
Matches 56; Conservative
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence;
2) imperfect repeats which are defined as 2 or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases;
3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dC-dA)n (dG-dT)n, or from at least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect This sequence is an example of a compound perfect repeat sequence of structure: (AC)20AG(AGAC)5AGA.

Sequence 65 BP; 33 A; 25 C; 7 G; 0 U;
                                                                                                                                                     having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g. paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf22 which contains the repeat sequence having the formula: (AC)20AG(AGAC)5AGA
                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Disclosure; Column 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T65724 standard: DNA; 65 BP. T65724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat sequence from polymorphic marker clone Mfd22.

Polymorphism; repeat sequence; genetic marker; primer; amplification; POLY; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-042299/04.
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  882
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                                                                            1.18;
Local Similarity 91.88;
ses 56; Conservative
                    ACACACACACACACACACACACACACACACACACACAGAGAGAGAGAGAGAGAGAGAC 940
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                                                                          Score 46; DB 29;
Pred. No. 5.09e-11;
0; Mismatches 4
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Pred. No. 5.09e-11;
0; Mismatches 4
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Search completed: Thu Mar 11 22:32:01 1999 Job time: 1409 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:01:32 1999; MasPar time 16.46 Seconds 455.994 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-866-354-36 (1-464) from US08866354.pep 3386 1 MILANVECLEFELDDTLRSL.....RARPSAALTVLSVLMLKLAL 464

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 .28:part28
29:part29

Statistics: Mean 34.889; Variance 136.192; scale 0.256

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 3 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
333 355 1554 1555 1455 762 782 782 782 999 999 999	Score
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Human Ret ligand RetL Rat glial cell line d Rat Ret ligand RetLI. Rat glial cell derive Human glial cell line Human Ret ligand RetL Human Ret ligand RetL Mouse Ret ligand RetL Mouse Ret ligand RetL Mouse Ret ligand RetL Human betafil viewer Reta Beta 3 adrenergic rec Human beta 3 adrenergy	Description
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91 2.7 342 2 R12090 Antigenic cystein pro 2.97e+01 93 2.7 485 3 R15508 Tomato ACC synthase e 2.09e+01 88 2.6 227 1 P94807 PBIwmj2 HIV fusion protein PB 4.98e+01 89 2.6 325 19 R91347 Murine PLAP, for redu 4.19e+01 89 2.6 325 17 R5872 WD-40 domain-contg. P 4.19e+01 89 2.6 362 19 W02667 G-protein coupled hum 4.1e+0.19e 19	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19
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WO9740152-A1.
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                                                                                                                            15-APR-1997; U06281.
14-APR-1997; US-837199.
22-APR-1996; US-015907.
09-MAY-1996; US-017221.
                                                                                                                                                                                                                                                                                                                                                                      Rat glial cell line-derived neurotrophic factor receptor. Rat; glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
                                               (AMGE-) AMGEN INC.
Fox GM, Jing S, Wen
WPI: 97-535836/49.
                                                                                                                                                                                                                                                                                                                      gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W35334 standard; Protein; 468 W35334;
                                                                                                                                                                                                                15-APR-1997;
                                                                                                                                                                                                                                                                                                                                               Huntington's disease; glaucoma; retinal degeneration; hearing loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1998 (first entry)
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neurotrophic factor receptor

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W37457 standard; W37457; 21-MAY-1998 (fi

(first entry)

Protein;

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Rat Ret ligand RetL1.
Ret ligand; RetL; RetLl; receptor; signal transduction; cell growth; renal cell; nerve cell; renal failure; nep

nephritis;

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CC disease or amyotrophic lateral sclerosis, complications of diabetes of disease or amyotrophic lateral sclerosis, complications of diabetes cand Huntington's disease and (optionally in combination with GDNF) glaucoma, retinal degeneration and hearing loss caused by injury to compare ear sensory neurons. The receptor can also be used to block cunwanted GDNF activity, analyse GDNF related molecules and stabilise GDNF activity, analyse GDNF related molecules and cells, preferably transfected ex vivo, can be used similarly by cc implantation, and the use of the receptor CNA in gene therapy is complantation, and the use of the receptor CDNA in gene therapy is complantation, and the use of the receptor CDNA in gene therapy is complantation, and the use of the cDNA can be used to identify complantation, and the probes based on the cDNA can be used to identify complantation, and to isolate molecules, e.g. to identify patients who complete the complex with the cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor complex of the receptor complex with the cDNA and animal complex with the cDNA and anim
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Matches 22
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Alzheimer's disease
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Local Similarity 48.2%;
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E--LTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLK-LA
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Pred. No. 2.14e-152;
102; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            principle (edlis protein comprises rat Ret ligand (RetL) RetL, a key component Claim 2: Page 49-51: 113pp; English.

Chaim 3: Page 49-51: 113pp; English.

Chaim 3: Page 49-51: 113pp; English.

Chaim 3: Page 49-51: 113pp; English.

Chaim 4: Page 49-51: 113pp; English.

Chaim 4: Page 49-51: 113pp; English.

Chaim 5: Page 49-51: 113pp; English.

Chaim 6: Page 49-51: 113pp; English.

Chaim 7: Page 49-51: 113pp; English.

Chaim 6: Page 49-51: 113pp; E
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27-NOV-1997.
07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding ret receptor ligands and related prote - vectors, transformed cells and antibodies, used for promoting growth and improving survival of injured cells, especially renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; meningitis; myelopathy; Creutzfeldt-Jakob disea cranilal nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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neurodegeneration; motor neurone disease; multiple sclerosis;
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Similarity 48.2%;
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468 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1554; DB 28; Pred. No. 2.14e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 120;
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                                                                           pri useful to develop products to diagnose and treat associated fisorders, particularly enteric nervous system or kidney disorders of claim 1; Page 78-79; 100pp; English.

Claim 2; Potein comprises full-length rat glial cell derived for the receptor applied factor receptor alpha (BDNFR alpha), a novel green for gDNF its amino acid sequence was deduced from an isolated cDNA clone (see T84975). The invention related to novel uses of GDNF and its receptor. In particular, it convel uses of GDNF and its receptor. In particular, it could not the general page was additional and antibodies which bind to the GDNFR alpha, solution as an invention of the general page was additional and antibodies. It also relates to assay systems for detection the GDNFR alpha, systems for studying the physiological rolution of the general page was an included for identifying molecules homologous to GDNFR alpha, and the reader control to the treatment of GDNF-related control and gone in the gone general page (claimed) for the treatment of GDNF-related control and gone in the conditions and gone in the conditions and gone in the conditions.
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat glial cell derived neurotrophic factor receptor alpha; GDNFR alpha; GDNF; rat; kidney disease; glomerulonephritis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                            Klein RD, Moore MW, Rosenthal A, WPI; 97-470819/43. N-PSDB; T84975.
               related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage_site
                                 associated with glomerulonephritis and enteric nervous system related disorders. Transgenic and knockout animals are also
                                                                and GDNFR alpha-related conditions, particularly kidney disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pnyvdss-s-1svapwcdcsnsgndledclkflnffkdntclknaiqafgngsdvtmwrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTNVNVSPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-618236.
US-615902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "0-glycosylated" 428..430
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349
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25..445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "extracellular domain"
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468 AA

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FLDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-

70 60

12

Matches Query Match

Local

Similarity

45.9%; llarity 48.2%; Conservative

102;

Score 1554; DB 27; Pred. No. 2.14e-152; l02; Mismatches 120;

Length Indels 18;

Gaps

15;

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14-APR-1997; US-837199.
22-APR-1996; US-015907.
09-MAY-1996; US-017221.
                                                                                     Claim 1; Pages 91-93; 196pp; English.

The present sequence is the human glial cell line-derived neurotrophic factor (GDNF) receptor, which can be used to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) glaucoma, retinal degeneration and hearing loss caused by injury to inner ear sensory neurons. The receptor can also be used to block unwanted GDNF activity, analyse GNNF related molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
Fox GM, Jing S, Wen D;
WPI: 97-535836/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human glial cell line-derived neurotrophic factor receptor. Human; glial cell line-derived neurotrophic factor; GDNF; recepto treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W35333 standard; Protein; W35333; 01-MAY-1998 (first entry)
stabilise GDNF in pharmaceutical formulations. Receptor expressing cells, preferably transfected ex vivo, can be used similarly by implantation, and the use of the receptor cDNA in gene therapy is
                                                                                                                                                                                                                                                                                                                                                                             treat dopaminergic nerve
Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                Glial cell line derived neurotrophic factor receptor - useful treat dopaminergic nerve cell disorders, e.g. Parkinson's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T88419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's disease; glaucoma; retinal degeneration; hearing loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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E--LTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLK-LA 463
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afpvqtttattttalrvknkplgpagseneipthvlppcanlqaqklksnvsgnthlcis

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1.J

PNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTNVNVSPK

GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFT

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ELTTNIIP-GSNKVIKPNSGPSRARPSAALTVLSVLMLKLAL ngnyekeglgasshittks-ma-appscglspllvlvvt-al 455

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                                                                                                                                                                                                                                                                                                                                                                                                                                          also contemplated. Probes based on the cDNA can be used to identify GDNF responsive cells and tissues, e.g. to identify pathents as would benefit from GDNF therapy, and abnormalities in receptor expression, and to isolate molecules that form a complex with the cDNA and animal complex with the cDNA or are homologous/cross-reactive with the cDNA and animal models that overexpress the receptor can be used to study the biological function of GDNF, knockout transgent animals can be used to detect GDNF dependent neurons or processes and the antibody can be used in immunoassays for the receptor. The receptor binds GDNF specifically and with high affinity, acting as part of a increasing depamine uptake in depaminergic cells.
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
               299
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EKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTYTSCPADNYQACLGSYAGMIGFDMT
                                                              ekpnclnlqdscktnyicrsrladfftncqpesrsvssclkenyadcllaysgligtvmt
                                                                                                            REISPTERCNRRKCHKALROFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYEDK
                                                                                                                               tsvs-ndvcnrrkchkalrqffdkvpakhsygmlfcscrdiacterrrqtivpvcsyeer
                                                                                                                                                                            PYEPVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICN
                                                                                                                                                                                               TM----LANK-ECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEAS
                                                                                                                                                                                                                                                                                                            FLDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-
                                                                                                                                                                                                                                                                                                                                                                               222;
                                                                                                                                                                                                                                                                                                                                                                                               44.98;
Similarity 48.18;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                               101;
                                                                                                                                                                                                                                                                                                                                                                                               Score 1520; DB 28;
Pred. No. 1.09e-148;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 465;
                                                                                                                                                                                                                                                                                                                                                                               Indels 17;
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                                                                                                                                                                              186
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Homo sapiens.
W09744356-A2.
27-NOV-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-013000.
16-JUL-1996; US-021859.
                                                                                                                       Human Ret ligand RetL1.

Ret ligand; RetL; RetL1; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrom; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                       r 6
W37459 standard; Protein;
                                                                                                                                                                                                                                                                                  W37459;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:03:59 1999; MasPar time 23.85 Seconds 728.716 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence:

>US-08-866-354-36 (1-464) from US08866354.pep 3386 1 MILANVECLEFFLDDTLRSL.....RARPSAALTVLSVLMLKLAL 464

Scoring table: PAM 150 Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: pir58 1:pir1 2:pir2 3:pir3 4:pir4 Mean 46.701; Variance 78.241; scale 0.597

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						16															ш	Result
90	92	92	92	91	93	90	93	91	91	91	91	90	95	95	96	96	95	03	00	00	782	Score M
		2.7				2.7		2.7	2.7		2.7			2.8	2.8	2 8		3 0			23.1	Query Match
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A57278	JQ1537	JQ1948	S17983	QRRTLD	TVRTTB	S74481	S62768	S67176	A57164	A44965	A45524	E69410	QRHUB3	QRHUBE	S72723	A47096	C70927	A38261	S62767	S68466	JE0082	₽
fibrillin-2 precursor	genome polyprotein 1	genome polyprotein l			nerve growth factor r	probable phosphoester	translation elongatio	isopentenyltra	major allergen Bla g	cysteine proteinase (cysteine proteinase (acetoin utilization p	beta-3-adrenergic rec	beta-3-adrenergic rec	dipeptide transport p		н	masking protein precu	translation elongatio	translation elongatio	GPI-linked receptor -	Description
	2.48e+0	2.48e+0		3.39e+0				3.39e+0		3.39e+00				9.54e-	6.90e-	6.90e-	9.54e-	6.65e-	1.84e-	1.84e-	1.79e-	Pred. No

45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ω ω	32	31	30	29	28	27	26	25	24
87	88	89	89	89	87	88	88	89	89	89	88	89	87	88	88	88	88	88	88	89	89
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2918	2871	2703	1408	1404	1115	925	863	854	808	790	621	503	493	480	463	432	418	379	379	354	325
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A54105	A55567	A24420	S16148	A36666	S64101	A39216	S41984	QRHYLD	VGBESM	TVHUTT	S26691	S23741	JC5621	S60381	A26652	DEMZMC	G02953	I57459	A44473	B56392	A40963
fibrillin-2 precursor	fibrillin I - boving	notch protein - fra:	gene serrate protoin	serrate protein prace.	PAN2 protein - yeast	plasma cell membrane		LDL receptor precurso		nerve growth factor r	serine proteinase (EC	hypothetical TPR/TRK	epidermal growth fact	RPD3 protein homolog	type I site-specific		beta-3-adrenergic rec	galactose-1-phosphate	UTPhexose-1-phospha	beta-galactoside alph	phospholipase A2-acti
	٠.			;	3.17.	я. 50 гг.	8.500	5.27.	6.270+00	6.276+111	8.500	6.27,	1.150.00	8.50e-0	8.50e+00		8.500+04	8.500-0	8.50e+0	6.27e+00	6.27e+00

ALIGNMENTS

Qy 215 YTYRMLFC	Db 208 HAQGLLLC	Qy 155 SAKSNHCI	Db 153 KPDSDLCI	Qy 96 KRGMKKEI	Db 101 HRRMKHQP	Db 41 CTQARKKC : Qy 40 CVRANELC	Query Match Best Local Similarity 38.2% Matches 123; Conservative	SUMMARY #	1-25 380-397 92,145,306	S	##residues ##residues ##cross-refe COMMENT This procesure	#accession	#title %	rs	ACCESSIONS :	ORGANISM		1
YTYRMLFCSC-QDQA-CAERRRQTILPSCSYEDKEKPNCLDLRGVCRTDHLCRSRLADFH 272	LPS-VT	SAKSNHCLDAAKACNINDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFDRVPSE 214	KPDSDLCLKFAMLCTLHDKCDRLRKAYGEACS-GIRCQRHLCLAQLRSFFEKAAES 207	KRGMKKELQCLQIYMSIHLGLTEGE-EFYEASPYEPVTSRLSDIFRLASIFSGTGADPVV 154	HRRWKHQATCLDIYWTVHPARSLGDYEL-DVSPYEDTVTSKPWKM-NL-S-K-LN-ML 152	CTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC 100 : :	23.1%; Score 782; DB 2; Length 397; larity 38.2%; Pred. No. 1.79e-154; Conservative 78; Mismatches 96; Indels 25; Gaps 18;	#length 397 #molecular-weight 44307 #checksum 2962	#admain signal sequence #status predicted #label Sity, #region hydrophobic\ #binding_site carbohydrate (Asn) (covalent) #status predicted		##motecute_type mkwa ##residues 1-397 ##label NOM ##cross-references DDBJ:AB008833; NID:g2627159; PID:g2627160 ##CTOSS-references DDBJ:AB008833; NID:g2627159; PID:g2627160	novel cDNA related to GDNFRalpha and NTNRalpha.	Molecular cloning and expression analysis of official analysis of official and expression analysis of official and expression analysis of official analysis of	Nomoto, S.; Ito, S.; Yang, L.X.; Kluchl, K.	JE0082 JE0082	#formal_name Mus musculus #common_name house mouse 21-May-1998 #sequence_revision 29-May-1998 #text_change	#type complete GPI-linked receptor • mouse GFBI-hha-3	

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#authors
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184-187
219-221
73,74,110,184,185,
187,219
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##molecule_type protein
57-65;239-270;352-361 ##label WES
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p_position 16p12-16p11.2
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##experimental_source liver
it is uncertain whether Met-1 or Met-4 is the
##note
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Local Similarity 27.6%;
hes 21; Conservative
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                                                                                                                                                                                                                                                                     LGLTEGEEFYEA-SPYEPVTSR-LSDIFRLA--SIFSGTGADPVVSAKSNH-CLDAAKAC 168
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                                                $62767 #type complete
translation elongation factor EF-Tu precursor - human
#formal_name Homo saplens #common_name man
24-Aug-1996 #sequence_revision 13-Mar-1997 #text_chang
28-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *superfamily translation elongation factor Tu; translation elongation factor Tu homology GTP binding; mitochondrion; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wells, J.; Henkler, F.; Leversha, M.; Koshy, R.
FEBS Lett. (1995) 358:119-125
A mitochondrial elongation factor-like protein is
over-expressed in tumours and differentially expressed
normal tissues.
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#length 452 #molecular-v
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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#region GTP-binding NKXD motif\
#region GTP-binding SAK/L motif\
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٧.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                #molecular-weight 49533 #checksum 1798
Burkhart,
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Σ:
Spremulli,
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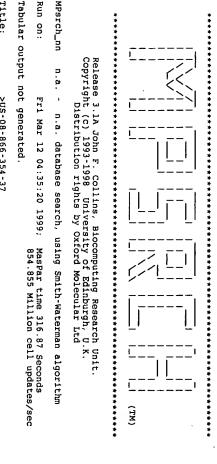
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58-184
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Best Local 9
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Best Local :
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219-221
70,71,107,181,182,
184,219
                                                                                                                                                                                                                                                                                                                                                                                              #authors Tsuji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8835-8839
Molecular cloning of the large subunit of transforming orcover.
#title factor type beta masking protein and expression of the mkNA in various rat tissues.
#cross-references MUID:91062373
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                                                                                                                                                   1032 DECLOP-KVCT-NGSCTNLEGSYMCSCHKGYSPT-P-DHRHCQ 1070
                                                                                                              159 NHCLDAAKACNINDNCKKIRSSYISICNREISPTERCNRRKCH
                                                                                                                                                                                                                                                                  ##residues 1 1-1712 ##label TSU
##cross-references GB:M55431; NID:g207285; PID:g207286
##cross-references GB:M55431; NID:g207285; PID:g207286
##CFICATION #superfamily LDL receptor ligand-binding repeat homology
#length 1712 #molecular-weight 186598 #checksum 9047
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                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
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                                                                                                                                                                                         h 3.0%;
Similarity 34.9%;
15; Conservative
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Similarity 27.6%;
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta (1995) 1264:347-356
Cloning, sequence analysis and expression of mammalian
mitochondrial protein synthesis elongation factor Tu.
S62767
C70927 #type complete probable rplS protein - My H37RV)
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#region GTP-binding NKXD motif\
#region GTP-binding SAK/L motif\
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                                                                                                                                                                                                                                                                                                                                                                preliminary
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1 452 #molecular-weight 49540
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Pred. No. 1.84e-01
19; Mismatches 3
                                                                                                                                                                                       Score 103; DB 2;
Pred. No. 6.65e-02;
12; Mismatches 12
                   Mycobacterium tuberculosis (strain
                                                                                                                                                                                           12;
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ORGANISM

l_name

Mycobacterium

tuberculosis



Title: Tabular output >US-08-866-354-37

Description: Perfect Score: Sequence: (1-1991) from US08866354.seq 1 CAAGTCAAAGGTTTAATCAT..... CAAGTCAAAGGTTTAATCAT.....CATGATTAAACCTTTGACTG
GTTCAGTTTCCAAATTAGTA....GTACTAATTTGGAAACTGAC

1991

Scoring table:

TABLE Gap 6

default

Nmatch

STD

Dbase 0; Query

188442 segs, 68026449 bases ×

Post-processing: Minimum Listing first 45 summaries

Database:

n-geneseq32 i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part22 23:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part27 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38 39:part39 40:part40

Statistics: Mean 9.638; Variance 5.919; scale 1.628

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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41 42	4.4 11	48 48	52	0 20	804	809	1169	1490	Score
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Human MDNCF antisense Human Ret ligand retL Human glial cell line	brain spec	ain spe	oding Gr	tandem r	DNA seg	DNA sequenc	onstituen	ıylase gei	f the M3/6 gen	nterl	DNA sequenc	ic DN		Ŋ	Generic DNA sequence	DNA	DNA 9	DNA	DNA s	1c DNA	Ņ	en	DŅ	DNA	Generic DNA sequence	t ligand re	O	Generic DNA sequence
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ALIGNMENTS

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07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Ret ligand retL3 cDNA.

Ret ligand; RetL; RetL3; receptor; signal transduction; human: cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome: cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                       nerve cells

Claim 1; Page 82-84; 113pp; English.

This sequence comprises cDNA encoding human Ret ligand (RetL (see w37463), a key component of the Ret signalling pathway.

a composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250), obtained from the composite of partial clone GJ148 (see v00250).
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Cate RL, Hession C,
WPI; 98-018431/02.
                                                                                                                                                                                                             New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting religions than dimproving survival of injured cells, especially renal or
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27-NOV-1997.
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llarity 99.9%;
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Pred. No. 0.00e+00;
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ID V00250 standard; cDNA; 1271 BP.

AC V00250;

AC V00250;

DT 21-MAY-1998 (first entry)

DE Human Ret ligand retL3 partial cDNA clone GJ128.

KW Ret ligand, RetL; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; www. cell growth; renal cell; nerve cell; renal failure; nephritis; www. kidney transplant; toxic injury; hypoxic injury;

KW cell growth; renal cell; nerve cell; renal failure; nephritis; we infection; meningitis; myelopathy; Creutzfalt-Jakob disease; will file sclerosis; www. infection; meningitis; myelopathy; Creutzfalt-Jakob disease; www. cranial nerve injury; spinal cord injury; Down's syndrome; www. cranial nerve injury; spinal cord injury; Down's syndrome; www. cranial nerve injury; spinal cord injury; Down's syndrome; www. cranial nerve injury; spinal cord injury; Down's syndrome; www. cranial nerve injury; spinal cord injury; syndrome; www. cranial nerve injury; syndrome; www. cranial n

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CC This sequence comprises a partial CDNA clone, designated GJ128, CC for human Ret ligand (RetL) RetL3 (see W37462), a key component of the Ret signalling pathway. It was isolated from a human adult CC heart cDNA library using a probe derived from a mouse retL3 partial CC cDNA (see V00256). A full-length sequence (see V00245-51). Vectors cretL3 CDNA has also been obtained, as well as rat and human retL1. CC human retL3 DNA and prokaryotic or eukaryotic host cells containing retL3 DNA and prokaryotic or eukaryotic host cells cransformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and cretL3 components with a toxin, imageable compound or radionuclide. CC RetL3, optionally when expressed from vectors in vivo, is used to component failure, nephritis, kidney transplants, toxic or hypoxic crenal failure, nephritis, kidney transplants, toxic or hypoxic crenal failure, nephritis, kidney transplants, toxic or hypoxic crenal nerve or spinal cord injury, developmental disorders such cc cranial nerve or spinal cord injury, developmental disorders such cc partipheral nervous system (Lyme disease, muscular dystrophy and cc ctc. to Ret-expressing cells, especially tumours.

Sequence 1271 BP; 264 A; 414 C; 316 G; 277 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.7%;
Best Local Similarity 99.7%;
Matches 1172; Conservative
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Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding ret receptor ligands and related prote vectors, transformed cells and antibodies, used for promoting ogrowth and improving survival of injured cells, especially renal
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07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
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Pred. No. 0.00e+00;
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Claim 1; Page 75-77; 113pp; English.

Crack 13 (see W37461), a key component of the Ret Signalling pathway.

Crack 14 (see W37461), a key component of the Ret Signalling pathway.

Crack 15 (see W37461), a key component of the Ret Signalling pathway.

Crack 15 (see W37461), a key component of the Ret Signalling pathway.

Crack 15 (see W37461), a key component of the Ret Signalling pathway.

Crack 16 (see W37457) and from the Signal Individual seed to the Signal 
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Best Local Similarity
Matches 1039; Conser
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New nucleic acid encoding ret receptor ligands and related proteins

- vectors, transformed cells and antibodies, used for promoting cel.

growth and improving survival of injured cells, especially renal or
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Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
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Pred. No. 0.00e+00;
0; Mismatches 224
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v00256;
21-MAY-1998 (first entry)
21-MAY-1998 (first entry)
Mouse Ret ligand retL3 cDNA partial clone (EST AA50083).

Ret ligand; RetL; RetL3; receptor; signal transduction; mouse cell growth; renal cell; nerve cell; renal failure; nephritis kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; bown's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.

ion; mouse;
nephritis;

V00256 standard; cDNA; 1878

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W09744356-A2. 27-NOV-1997.

musculus

Location/Qualifiers 205..1245

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Matches 103
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel M. WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 71-73; 113pp; English.

This sequence comprises EST AAO50083, identified as a partial cDr
for mouse Ret ligand (RetL) RetL3 (see W37455), by sceening of
an EST database with rat RetL1 (see W37457). A full-length
mouse retL3 cDNA clone (see V00249) was obtained by combining
AAO50083 with a clone obtained by 5'RACE. Rat, mouse and
human retL1, retL2 and retL3 cDNA sequences (see V00245-51) and
encoded polypeptides (see W37457-63) are claimed and can be used
in methods for promoting cell growth and improving survival of
cells, especially renal or neural cells.

Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth and improving
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New nucleic act
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 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid encoding ret receptor ligands and related prote ectors, transformed cells and antibodies, used for promoting with and improving survival of injured cells, especially renal
                                          ctcabaccagactcggacctctgcctcabatttgctatgctgtgtactcttcacgacaag
                                                                                                                                                                                     ccctatgaagacacagtgaccagcaaaccctggaaaatgaatcttagcaagttgaacatg
                                                                                                                                                                                                                                  aacagctctctgatagactgcaggtgccatcggcgcatgaagcaccaagctacctgtctg
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                                                                                                                                                                                                                                                                                                                                                                                           cccgcttgcaaggctgcctaccagcacctgggctcctgcacctccagt-taagcaggccg
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CTGCTACTGTGCCCATGTGCCCCCAACGACCGGGGCTGCGGGGGAGCGCCGGCGCAACACC
            AACAGCTCTGATAGGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTGCTTG
                                                                                                                                                                                                                                                                                                                                  CTGCCCTCAGAGGAGCCTTCGGTCCCTGCTGACTGCCTGGAGGCAGCACACTCAGG
                                                                                                                                                                                                                                                                                                                                                                               CCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTGCACCTCTAGCATAAGCACCCCA
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al Similarity 82.2%;
1039; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 804; DB 39; I
Pred. No. 0.00e+00;
0; Mismatches 223;
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21-MAY-1998 (first entry)

Runan Ret ligand retl3 partial cDNA clone GJ128.

Ret ligand; RetL3; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal fallure; nephritis: kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis: infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                                                                                                                     Homo sapiens.
Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcttctcccaggactgggcagactctactttttcagtggtgcagcagcagcagcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTTTCACAGCCAA
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                                                                                                           Location/Qualifiers
2..946
/*tag= a
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W09744356-A2.
27-NOV-1997:
07-MAY-1997:
10-APR-1997:
08-MAY-1996:
08-017427.
07-JUN-1996:
08-019300.
16-JUL-1996:
08-021899.
(BIOJ) BIOGEN INC.
Cate RL, Hession C, Sani.
WPI; 98-018431/02.
P-PSDB: W37462.

Sanicola-Nadel

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So sequence 1271 Bp; 264 A; 414 C; 316 G; 277 T;
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Best Local s
Matches 8
                                                                                                                 27-NOV-1997.

07-MAY-1997; U07726.

10-APR-1997; US-017427.

08-MAY-1996; US-017427.

07-JUN-1996; US-019300.

16-JUL-1996; US-021859.
                                       (BIOJ) BIOGEN INC.
Cate RL, Hession C, S
WPI; 98-018431/02.
P-PSDB; W37463
                                                                                                                                                                                                                                                                                                                      Human Ret ligand rett3 cDNA.

Ret ligand; RetL; RetL3; receptor; signal transduction; human;
cell growth; renal cell; nerve cell; renal failure; nephritis;
kidney transplant; toxic injury; hypoxic injury;
neurodegeneration; motor neurone disease; multiple sclerosis;
infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
cranial nerve injury; spinal cord injury; Down's syndrome;
cerebral palsy; Lyme disease; muscular dystrophy;
myasthenia gravis; tumour; therapy; ss.
Homo saplens.
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Claim 1; Page 79-80; 113pp; English
This sequence comprises a partial co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1998 (first entry)
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       vectors,
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 nucleic acid encoding ret receptor ligands and related proteins actors, transformed cells and antibodies, used for promoting cel
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82; Conser
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                                                                                                                                                                                                                                                                            Location/Qualifiers 175..1377
                                                                                                                                                                                                                                                         /*tag=
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98.8%;
                                                                                 Sanicola-Nadel
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Pred. No.
0; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse RetL3 sequences are also claimed (see W37457-62). Vectors are containing retL3 bNA and prokaryotic or enkaryotic host cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and fusion proteins with a toxin, imageable compound or radionuclide. RetL3, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis). Fusion proteins are used to deliver toxins etc. to Ret-expressing cells, especially tumours.
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Best Local S
Matches 8
                                                                                                      27-NOV-1997. U07726.
07-MAX-1997; U07726.
10-APR-1997; US-017427.
08-MAX-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
(BIOJ ) BIOGEN INC.
Cate RL, Hessian C, Sanicola-Nadel M;
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                 Mouse Ret ligand reti3 cDNA partial clone (EST AA50083). Ret ligand; RetL; RetL3; receptor; signal transduction; mouse; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
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Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence comprises cDNA encoding human Ret ligand (Re (see W37463), a key component of the Ret signalling pathwe a composite of partial clone GJ148 (see V00250), obtained adult heart cDNA library, and of clone GJ135, isolated from adult spinal cord cDNA library. Rat and human Retil, human adult spinal cord cDNA library.
                                  New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting (e) growth and improving survival of injured cells, especially remained of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W37465
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Claim 1; Page
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                     nerve cells
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82; Conser
 Page
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                                                                                                                                                                                                                                                                                                      Location/Qualifiers 205..1245
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     71-73;
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113pp;
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0; - Mismatches
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5.61e-33;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Fr1 Mar 12 03:17:56 1999; MasPar time 2882.03 Seconds 1237.127 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-866-354-37 (1-1991) from US08866354.seq 1991

1 CAAGTCAAAGGTTTAATCAT......CATGATTAAACCTTTGACTG 1991 GTTCAGTTTCCAAATTAGTA......GTACTAATTTGGAAACTGAC

Scoring table: TABLE default Gap 6

Nmatch

STD :

Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est56

Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
genbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est2 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics:

Mean 11.743;

Variance 2.290; scale 5.129

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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13	12	11	10	9	8	7	σ	IJ	4	ω	N	-	NO.
158	160	160	160	181	232	289	332	352	358	389	428	454	Score
7.9	8.0	8.0	8.0	9.1	11.7	14.5	16.7	17.7	18.0	19.5	21.5	22.8	Query Match
350	474	396	373	189	465	442	350	436	373	396	450	474	Length
15	11	11	11	1	21	22	5	21	11	1	21	11	BB
AA984036	AA694259	AA687725	AA678356	AA676213	AA050083	AA049894	AA984036	W69813	AA678356	AA687725	W69774	AA694259	ID
oq02f02.s1	. 81	6.81	zi25g01.s1	zi39h12.s1	mj08d05.rl	mj11d08.r1	. 81	. r1	z125g01.s1	. 81	zd48g06.s1	. zi31d11.s1	Description
NCI_CGAP_Lu	Soares feta	NCI_CGAP_Pr	Soares feta	Soares feta	Soares mous	Soares mous	NCI_CGAP_Lu	Soares feta	Soares feta	NCI_CGAP_Pr	Soares feta	Soares feta	
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Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free thr This clone is available royalty-free thr IMAGE Consortium (info@image.lini.gov) f Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 451. Location/Qualifiers source 1. 474	MAITIMEN, D., KUCADA, T., LACY MAITIN, J., MOORE, B., Schell Theising, B., White, Y., Wyli TITLE WashU-NCI human EST Project JOURNAL Unpublished (1997) COMMENT Contact: Wilson RK	SOURCE human. ORGANISM Homo sapiens Eukaryotae; Metazoa; (Frimates; Catarriini; Primates; 1 to 474) AUTHORS Hillier,L. Allen,M. Krizman,D. Kucaba,T.	DOCUS AA694259 DEFINITION zi31d11.s1 Soares fet clone 432405 3', mRNA ACCESSION AA694259 NID 92695197 KEYWORDS EST.
Contact: wilson kk Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Email: est@watson.wustl.edu This clone is available royalty-free through LLNL: contact : "" IMAGE Consortium (info@image.llnl.gov) for further informar: -40m13 fwd. ET from Amersham	KILEMAN, J., KUCADA, T., LACY, M., Le, N., Lennon, G., MARTA, M., MARTIN, J., MOORE, B., Schellenberg, K., Steptoe, M., Tan, F., Thelsing, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997) Contact: Wilson RK	human. Homo sapiens Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 474) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacv, M., Le, N., Lennon, G., Marra, M.	AA694259 474 bp mRNA EST 16-DEC-1997 zi3ld11.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone 432405 3', mRNA sequence. AA694259 g2695197 EST.

with a Pac I – oligo(dT) primer [5′

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343930 3',
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                                                    Homo sapiens
Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/lab_host="DH10B (ampicillin resistant)"
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/clone="432405"
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/sex="male"
                                                                                                                                                                                                                                                                mRNA sequence
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Soares fetal heart NbHH19W
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99.6%;
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Pred. No. 0.00e+00;
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Local Similarity 98.7%;
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AATGANGACTGGACCAGTAAGGATCTGG
                                                                                     AGTCAAGAGGAAGGGCTCACAAAGGGGGCTTGGTGGAGCTGGTCACCACCAGATG - ACATG
                                                                                                AGTCAAGAGGAAGGGCTCAGAAAGGGGCTTGGTGGAGCTGGTCACCACCACCAGATGGACATG
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                                     GCTAAATTGTGGCCACCAAGGAGGGCCAGCATGAATCAGAAGTGGAGATGGGGTGGAGGG
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Washu-Merck EST Project
Washington University Schoc
4444 Forest Park Parkway, E
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="19 weeks"
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Pred. No. 0.00e+00;
0; Mismatches 4
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                                                             ATTCTTCACAAAGGAGAATGACTTTCTAGGCTGCCTCAGAACACCCAGTCCTCCCTACCC 241
                                                                                                                   GGCAGTGCAGGCAGTAGTTTTCCATCCTCCACTCAGAGGAGGAGGAGGAGGAGC 1811
                                                                                                                                                                                                 CTTCTTCACAAAGGAGAATGACTTTCTAGGCTGCCTCAGAACACCCCAGTCCTCCCTACCC
                                                                                                                                                          GGCAGTGCAGGCAGTAGTTTTCCATCCTCCACTCAGAGGAGGAGGAGGAGGGGGGGAGGAGC 181
  TAACCCTAATCTGGAATGCAATAGAGAATGGCTAACTTATTAGATTCTGGTGATCCTGGT
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1 Similarity 99.2%;
392; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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nv08c06.sl NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219594,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vnote-"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was 1:gated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI stres of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="normal prostate"
/lab_host="DH10B"
91 c 111 g 78 t
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/clone="IMAGE:1219594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Pr22"
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                                                                                                                                                                                                                                                                                                                                                                              Score 389; DB 11;
Pred. No. 0.00e+00;
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AGTCAAAGGTTTAATCATGATCCAAGAGCCCCAGAGAGACTTTAGGACAATAATAGGAATA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact in Info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 365.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 373)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,N., Karizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,N., Martin,J., Woore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson. Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. i Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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                                                                                                                 Similarity
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                                                                                         18.0%;
larity 99.2%;
Conservative
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: Liver and Spleen: Vector: pT713D (fharm
with a modified polylinker; Site_1: pac I: Ste_2: Fo
This is a subtracted version of the original source
This is a subtracted version of the original source
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This is a subtracted version of the original source.
                                                                                                                                                                                                        /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
85 c 101 g 80 t
                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                    'clone_lib="Soares fetal liver spleen lNFLS
                                                                                                               Score 358; DB 11;
Pred. No. 0.00e+00;
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AAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGACAG 125

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                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 580 Std Error: 0.00
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo 1 (bases 1 to 436)
1 (bases 1 to 436)
1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Dubuque, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W69813 436 bp mRNA EST 1
zd48g06.r1 Soares fetal heart NbHH19W Homo sapiens
343930 5', mRNA sequence.
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Location/Qualifiers
                                     NbHL19W.
 /db_xref="taxon:9606"
/clone="343930"
                                                                                                                                                                                                                                /organism="Homo sapiens"
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Insert Length: 762 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 284.
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41 GGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTCCAGTCCTCATTCCCTCCACC
            Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.

Emmert_Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Second distribution: NCI-CGAP clone distribution infound through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGATCCTGCCGAACATCTGGGGCATCAGGA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                      AA984036 350 bp n
oq02f02.s1 NCI_CGAP_Lu5 H
mRNA sequence.
AA984036
g3162561
EST:
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                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mam
Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 350)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anat
                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                              Tumor Gene Index
www-bio.llnl.gov/bbrp/image/image.html
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Similarity 98.0%;
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/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 0.00e+00;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                      EST
                                                                     Unpublished (1996)
On Dec 31, 1996 th
                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
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75791 5', mRNA seguence.
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/clone_11b="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
a 81 c 73 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo /db_xref="taxon:9606"
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1. .350
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Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL: Contained
IMAGE Consortium (info@image.llnl.gov) for further inform MGI:286535
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/dev_stage="13.5-14.5dpc
/lab_host="DH10B"
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/clone="475791"
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/strain="C57BL/6J"
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CCCGCTTGCAAGGCTGCCTACCAGCACCTGGGCTCCTGCACCTCCAGT-TAAGCAGGCCG
                                    CCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGCTGAT
                                                                          CTGATGTTGCTGCTGCTGCCGCCGCCGCCGCCGCTCGCCAGCCGGAGACCCCCTT 304
                                                                                                                                CTGATGATCCTGCTACTGGTGCTGTCGTTGTGGCTGCCACTTGGAGCAGGAAACTCCCTT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA050083 465 bp mRNA EST 09-SEP-1996 mj08d05.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone 475497 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morrils, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
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quality sequence stop: 431.
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Location/Qualifiers
                                                                                                                                                                                        11.7%;
llarity 81.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated t Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

//db.xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                    /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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147 c
                                                                                                                                                                                      Score 232; DB 21;
Pred. No. 0.00e+00;
0; Mismatches 69
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Enther
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 189)
1 (bases 1 to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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                                                                                                                                                                                                                     /lab_host="DH10B (ampicillin
45 c 49 g 43 t
                                                                                              /sex="male"
                                                                                                                                /clone_lib="Soares fetal liver spleen lNFLS
                                                                                                                                                               /clone="433223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                'dev_stage="20 week-post conception fetus"
                                                                                                                                                                                             /db_xref="taxon:9606"
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Query Match

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Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 365.
Location/Qualifiers
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4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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1. (bases 1 to 373)
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                                                                                                                   107
                                                                                                                                                                                                                                                                                             /Organism="Homo sapiens"
/Organism="Homo sapie
                                                                                                       /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
85 c 101 g 80 t
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Length 373;
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                     Query Match
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Matches 169; Conservative
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Br
Emmert_Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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High quality sequence stop: 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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1 (bases 1 to 396)
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AA687725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
                   Similarity
                                                                                                      116
                                                                                                                                                                                                                                           /note="Organ: prostate: Vector: pT7T3D-Pac (Pharma with a modified polylinker; 1st strand cDNA was production normal prostate bulk tissue, and was then prime of a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), diseased with N I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonald."
                                                                                                  /tissue_type="normal prostate"
/lab_host="DH108"
91 c 111 g 78 t
                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:1219594"
                                                                                                                                                                /sex-"male"
                                                                                                                                                                                 /clone_lib-"NCI_CGAP_Pr22"
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                   8.0%;
97.7%;
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Score 160; DB 11;
Pred. No. 2.26e-258;
0; Mismatches 3;
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                                      Length 396;
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AAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGACA 135
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1 (bases 1 to 474)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S. Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)
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AA694259
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EST.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 451.
Location/Qualifiers
                                                                                                              8.0%;
Similarity 97.7%;
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Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
100 c 137 g 103 t
                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="432405"
                                                                                                                                                                                                                                          /clone_lib="Soares fetal liver spleen lnFLS
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                                                                                                                                                                                                                           'sex="male"
                                                                                            Score 160; DB 11; 1
Pred. No. 2.26e-258;
0; Mismatches 3;
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                                        AAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGGG
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High quality sequence stop: 284.
Location/Qualifiers
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1 (bases 1 to 350)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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oq02f02.sl NCI_CGAP_Lu5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can lafound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement:
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                                                                                                                                                                                                                         7.9%;
Similarity 97.1%;
                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                           /Organism="Homo sapiens"
//note="Organ: lung: Vector: pT7T3D-Pac (Pharmacia) will
//note="Organ: lung: Vector: pT7T3D-Pac (Pharmacia) will
//note="Organ: lung: Vector: pT7T3D-Pac (Pharmacia) will
modified polylinker: 1st strand cDNA was prepared will
neuroendocrine lung carcinoid, and was then primed w
Not I - oligo(dT) primer. Double-stranded cDNA wild
to Eco RI adaptors (Pharmacia), digested with we
cloned into the Not I and Eco RI sites of the
pT7T3 vector. Library is normalized. Library
pT7T3 vector. Library is normalized. Library
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//lone="TMAGE:1585179"
//clone="the" NCI_CGAP_Lu5"
//tlssue_type="carcinoid"
//lab_host="DH10B"
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                            81
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                      Score 158; DB 15;
Pred. No. 3.06e-254;
0; Mismatches 4;
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122

GGGCAGTGCAGGCAGTAGTTTTCCATCCTCCATCCAGGGGAGGAG-CGAGGGG 173

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122 GGGCAGTGCAGGCAGTTGTTTTCCATCCTCCACTCAGAGGAGGAGGACGAGGGG 174
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                                                        62
                                                                                                                                                             Local
                                                                                 AAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGACA 121
                             AAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGGACA
                                                                                                                                            7.9%;
l Similarity 97.1%;
168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 450)
Hillar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project 
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zd48g06.sl Soares fetal h
343930 3', mRNA sequence.
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 /sex="unknown"
/dev_Stage="19 weeks"
/lab_host="DH10B {ampicillin resistant)"
/lab_host="DH10B \ (ampicillin resistant)"
complement(<1...>450)
g6 c 134 g 87 t 3 other;
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="343930"
                                                                                                                                                                                                                                                                                                                                         NbHL19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                           /clone_lib="Soares fetal heart NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450 bp mRNA EST Soares fetal heart NbHH19W Homo
                                                                                                                                         Score 158; DB 21; Li
Pred. No. 3.06e-254;
Pred. No. 3.06e-254;
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                                                                                                                                                                         Length 450;
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245 CTGATGTTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCCCCTT 304
                                                                                                     85 CTGATGATCCTGCTACTGGTGCTGTCGTTGTGGCCTGCCACTTGGAGCAGGAAACTCCCCTT 144
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Eukaryotae; mitochondrial eukaryotes; Metazoa: Chordonic
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMAX: 314 400 1012
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact in
This clone is available royalty-free through LLNL ; contact in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., VII. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, H. Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, I. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Lind, R. Li
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Location/Qualifiers
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                                                                                                                                                                                            7.6%;
larity 79.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="13.5-14.5dpc
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/clone="475095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism-"Mus musculus"
strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B"
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                                                                                                                                                                                            Score 152; DB 21;
Pred. No. 7.19e-242;
0; Mismatches 55;
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                                                                                                                                                                                                                                                           Length 353;
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在这种证明,我们的是我们的,我们的的,我们的的,我们的的,我们的的,我们的,我们的,我们的我们的的,我们的我们的,我们的,	[] [] [] [] [] [] [] [] [] [] [] [] [] [

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:13:58 1999; MasPar time 14.47 Seconds 447.378 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-866-354-38 (1-400) from US08866354.pep 3033

Sequence: 1 MVRPLNPRPLPPVVLMLLLL......PWVPSLFSCTLPLILLLSLW 400

Scoring table: PAM 150 Gap 11

Searched: 131922 segs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 12:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.299; Variance 146.727; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DВ	ID	Description	Pred. No.
1	3029	99.9	400	28	W37463	Human Ret ligand RetL	7.97e-287
2	2378	78.4	315	28	W37462	Ret ligand	1.80e-221
ω	2356	77.7	397	28	W37461		2.89e-219
4	2074	68.4	346	28	W37465	t ligand	.03e-
ۍ	717	23.6	460	28	W37459	Human Ret ligand RetL	1.74e-56
6	701	23.1	464	28	W37460	_	6.25e-55
7	686	22.6	465	28	W35333	Human glial cell line	1.79e-53
8	678	22.4	468	28	W37457	Rat Ret ligand RetLl.	1.07e-52
9	678	22.4	468	27	W27327	Rat glial cell derive	1.07e-52
10	678	22.4	468	28	W35334	Rat glial cell line-d	1.07e-52
11	532	17.5	346	28	W37458	Human Ret ligand RetL	1.31e-38
12	113	3.7	986	24	W25171	Human insulinoma-asso	1.09e+00
13	113	3.7	1015	27	W35345	Human protein tyrosin	1.09e+00
14	113	3.7	1015	23	W18092	Type I diabetes-assoc	1.09e+00
15	110	3.6	969	24	W25170	Human insulinoma-asso	1.83e+00
16	106	3. 5	1012	27	W35296	Macaque islet cell an	3.64e+00
17	101	ω . ω	102	13	R70793	Gro-beta/MIP-2-alpha.	8.48e+00
18	101	3.3	107	4	R23034	Human Gro beta cytoki	8.48e+00

9.76	G-CSF deriv. without	R13369	w			86	ij
	Chicken cytotactin.	R94563	16			88	4
_	Product of alternativ	R58911	11			87	ū
æ	Alternatively spliced	R87152	17			87	ົນ
œ	Inositol-1,4,5-tripho	W01596	20			87	1
œ	Protocadherin clone 4	R87146	17		•	87	6
œ	Human protocadherin-4	R58906	片			87	õ
8	A. niger strain M-62	R94370	19		•	87	ã
σ.	Canine herpesvirus gl	W23000	26	522	2.9	89	37
	MISR2A/MISR2B.	R41921	œ			89	õ
	Mullerian inhibiting	W03760	18			89	ភ
	Arabidopsis violaxant	W09876	22			87	4
	Sequence of insulin-l	R21833	4			87	ຜ
8.34e	•	R22209	4			87	ົວ
	Nuclear envelope-asso	R98744	19			90	ï
4.40e	Bordetella pertussis	W23278	24			91	õ
	Human acylcoenzyme A:	W43407	29			90	ÿ
	Human chemokine alpha	W36449	27			91	æ
2.700-	Serine/threonine kina	R70240	13			94	7
	Mouse Activin recepto	R55373	10			94	ð
-	ene pro	W03740	<u>.</u>			96	ŭ
	Miniature swine retro	W32098	25		٠	96	Ä
	Prostaglandin endoper	R21690	4			96	ü
	Tazarotene induced de	R98742	19		٠	98	Ñ
۵۱	ő	R55369	10		٠	101	ĭ
<u>.</u> ~	Human macrophage inil	R20589	4			101	õ
7.	10	R20529	4		•	101	ω

ALIGNMENTS

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RetL3, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis). Fusion proteins are used to deliver toxins etc. to Ret-expressing cells, especially tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                      W09744356-A2.
27-NOV-1997.
07-MAY-1997; US-017427.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
18-JUL-1996; US-021859.
                                                                                                                                                                           Human Ret ligand RetL3 partial sequence.

Ret ligand; RetL; RetL3; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
              Cate RL, Hession C
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                 W37462 standard; Protein;
W37462;
21-MAY-1998 (first entry)
                                                                                                                                                                  Ното
   N-PSDB;
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399; Conser
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                             Sanicola-Nadel
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Pred. No. 7.
0; Mismatc
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1.97e-287;
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Pri nerve cells

Proceding 2; Page 81-82; 113pp; English.

CC Intim 2; Page 81-82; 113pp; English.

CC This amino acid sequence comprises a human Ret ligand (RetL) RetL3

CC Quartial polypeptide sequence, deduced from a partial clone (see

CC (00250) isolated from a human adult heart cDNA library; a

CC full-length RetL3 sequence (see W37463) is also claimed, as well

CC (see W37455-61). Ret ligand is a key component of the Ret

CC (see W37455-61). Ret ligand is a key component of the Ret

CC (see W37455-61). Ret ligand is a key component of the Ret

CC (signalling pathway that specifically interacts with Ret receptor

CC (the Ret tyrosine kinase domain. Vectors containing retL3 DNA and

CC (the Ret tyrosine kinase domain. Vectors containing retL3 DNA and

CC (the RetL3, its soluble variants and fusion proteins with a toxin,

CC (imageable compound or radionuclide. RetL3, optionally when

CC (tissue and survival of damaged tissue, particularly kidney or

CC (tissue and survival of damaged tissue, particularly kidney or

CC (neural tissue. Typical applications are in renal failure,

neural tissue. Typical applications are in renal failure,

neural tissue or prion infections (e.g. meningitis, myelopathy

CC (associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or

spinal cord injury, developmental disorders such as Down's syndrome

CC system (Lyme disease, muscular dystrophy and myasthenla gravis),

CC (see dis, especially tumours.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
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Matches 30
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                                  thchpmdilgtcateqsrclraylgligtamtpnfvsnvntsvalsctcrgsgnlqeece
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                                                                                                                                                                                            tpqlrnssligcmchrrmknqvacldiywtvhrarslgnyeldvspyedtvtskpwkmnl
                                                                       THCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFASNVNTSVALSCTCRGSGNLQEECE
                                                                                                                                                                                  AQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNL 149
                                                                                                          PHAQGLLLCPCAPNDRGCGERRRNT IAPNCALPPVAPNCLELRRLCFSDPLCRSRLVDFQ
                                                                                                                                                                                                                        308;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                      78.4%;
larity 99.0%;
Conservative
                                                                                                                                                                                                                               Score
Pred.
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                                                                                                                                                                                                                     re 2378; DB 28;
d. No. 1.80e-221;
Mismatches 2;
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                                                                                                                                                                                                                      Indels
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RESULT
ID WI
AC WI
21.MAY.1998 (first entry)
Mouse Ret ligand RetL3:
Ret ligand; RetL3; receptor; signal transduction; mo cell growth; renal cell; nerve cell; renal failure; nephri kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple scleros infection; meningitis; myelopathy; Creutzfeldt-Jakob disea; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
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sclerosis: nephritis;

mouse:

disease:

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390

400

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CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3, CC deduced from cDNA clones (see Y00249) isolated from an EST CC deduced from cDNA clones (see Y00249) isolated from an EST CC deduced from cDNA clones (see Y00249) isolated from an EST CC deduced from cDNA clones (see Y00249) isolated from an EST CC deficiences (see W37457-60 and W37462-63) are also claimed. RetL1 is component of the Ret signalling pathway that specifically component of the Ret signalling pathway that specifically component of the Ret signalling Ret dimerisation cand/or autophosphorylation of the Ret tyrosine kinase domain. CC and/or autophosphorylation of the Ret tyrosine kinase domain. CC cells transformed or transfected with these vectors are claimed, as component of the retl3, its soluble variants and cells as amethod for production of RetL3, its soluble variants and cc well as a method for production of RetL3, its soluble variants and cc well as amethod for production of RetL3, its soluble variants and cc well as method for production of RetL3, its soluble variants and cc promote growth of new tissue and survival of damaged tissue, components yield the compound or reddimical decompositions are in cc injury, neurodegeneration, motor neurone disease, multiple sclerosis, components with HIV or Creutzfeldt-Jakob disease), cranial nerve or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC cells, especially tumours.
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Best Local S
Matches 30
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10-ARR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
(BIOJ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel MWPI; 98-018431/02.
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Mus musculus.
WO9744356-A2.
27-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Claim 2; Page 77-78; 113pp; English.
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                                                                                                                                                                                                LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFASNV
                                                                                                                                                                                                                                                                                                               PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNT IAPNCALPPVAPNC
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                                                                                    NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM
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larity 77.9%;
Conservative
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Pred. No. 2.89e-219;
53; Mismatches 31;
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RESULT
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W37459 standard;

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R 10-APR-1997; US-017427.

R 08-MAY-1996; US-017427.

R 07-JUN-1996; US-019300.

R 16-JUL-1996; US-019300.

R 16-JUL-1996; US-021859.

A (BIOJ) BIOGEN INC.

Cate RL, Hession C, Sanicola-Nadel M;

WPI; 98-018431/02.

R WPI; 98-018431/02.

R N-PSDB; V00256.

R N-PSDB; V00256
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Best Local
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W09744356-A2.
27-NOV-1997.
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This polypeptide comprises a partial sequence of mouse Ret 15:25.4 RetL3, deduced from EST AA050083 cDNA (see V00256). A full-16:25.4 mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse and human retL1, retL2 and retL3 cDNA sequences (see V00245-51) and encoded polypeptides (see W37457-63) are claimed and can be used in methods for promoting cell growth and improving survival of cells, especially renal or neural cells.
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Ret ligand; RetL; RetL3; receptor; signal transduction; mouse; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
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W37465;
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    371
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ISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIXWTVHRARSLGNYE 130
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                                                                                                                                                                    SVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVMAH
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Similarity 81.3%;
269; Conservative
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Pred. No. 5.03e-191;
35; Mismatches 25:
        400
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Claim 2; Page 64-66; 113pp; English.
CC Inim 2; Page 64-66; 113pp; English.
CC This maino acid sequence comprises human Ret ligand (RetL) RetL1,
CC deduced from cDNA clones (see v00247) isolated from a human
CC foetal kidney. Rat RetL1 and mouse and human RetL2 and RetL3
CC sequences (see w37457 and w37460-63) are also claimed. The
CC human RetL1 sequence is 93.3% identical to that of rat. Ret ligand
CC is a key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor, triggering Ret dimerisation and/or
CC containing retL1 DNA and prokaryotic or eukaryotic host cells
CC ctansionmed or transfected with these vectors are claimed, as well
CC transformed or transfected with these vectors are claimed, as well
CC transformed or transfected with these vectors are claimed, as well
CC prionally when expressed from vectors in vivo, is used to promote
CC proteins with a toxin, imageable compound or radionuclide. RetL1,
CC prionally when expressed from vectors in vivo, is used to promote
CC proteins with a toxin, imageable compound or radionuclide. RetL1,
CC prionally when expressed from vectors in vivo, is used to promote
CC proteins with a toxin, imageable compound or radionuclide. RetL1,
CC prionally when expressed from vectors in vivo, is used to particularly
CC kidney or neural tissue. Typical applications are in renal failure,
CC nephritis, kidney transplants, toxic or hypoxic injury,
CC kidney or viral or prion infections (e.g. meningitis, myelopathy
CC sociated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
Spinal cord injury, developmental disorders such as Down's syndrome
and cerebral palsy, or conditions involving the peripheral nerveus
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC clis, especially tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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27-NOV-1997.
07-MAY-1997:
U7-MAY-1997:
U7-MAY-1997:
U7-MAY-1997:
U7-MAY-1997:
U7-MAY-1997:
U7-MAY-1996:
U7-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cate RL, Hession C WPI; 98-018431/02.
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21-MAY-1998 (first entry)
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--CQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVA-PN
                                                                                                                                                                                                                                                   ye-pvnsrisdifrvvpfisvehipkgnncldaakacnlddickkyrsayitpcttsvsn 179
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                                                                                      dvcnrrkchkalrqffdkvpakhsygmlfcsc--rdiacterrrqtivpvcsyeerekpn
                                                                                                                                                                                           YEDTVTSKPWKM-NLSK-LNMLK-PDSDLCLKFAMLCTLNDKCDRLRKAYGEACS-G-PH
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                                                                                                                                                                                                                                                                                                                                                                                           -SEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSP
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llarity 36.5%;
Conservative
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40 cvranelcaaesncssryrtlrqclag-rdr-ntmlan--kecqaalevlqesplydcrc 95 CLQARRKCQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMC

Indels

25;

Gaps

18;

Matches

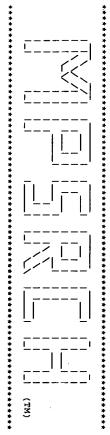
Similarity

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RESULTATION OF THE LANGE LANGE AND L
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                                                                                                                                                                Proceed of the sequence comprises human Ret ligand (Retl) Kolling: Page 69-70; 113pp; English.

CC This amino acid sequence comprises human Ret ligand (Retl) Kolling: This amino acid sequence (see V00248) isolated from a human i.n. CC deduced from a cDNA clone (see V00248) isolated from a human i.n. CC liver library. Rat and human Retll and human and mouse Retll. CC sequences (see W37457-59 and W37461-63) are also claimed. Human CC liver library. Rat and human Retll protein. Retl is a component of the Ret signalling pathway that specifically component of the Ret signalling pathway that specifically component of the Ret tyrosine kinase domain. CC wectors containing retl2 DNA and prokaryotic or eukaryotic host component or transferted with these vectors are claimed, as complete the compound or radionuclide. CC cells transformed or transfected with these vectors are claimed, as composite growth of new tissue and survival of damaged tissue, optionally when expressed from vectors in vivo, is used to compound growth of new tissue and survival of damaged tissue, can failure, nephritis, kidney transplants, toxic or hypoxic compound failure, nephritis, kidney transplants, toxic or hypoxic compound with HIV or Creutzfeldt-Jakob disease, multiple sclerosis, consociated with HIV or Creutzfeldt-Jakob disease, multiple sclerosis, consider such as Down's syndrome can decrebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC cells, especially tumours.

CC esting the peripheral nervous sequence 4464 AA.
                                          Query Match
Best Local
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
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RetL1; RetL2; receptor; signal transduction; human; Ret ligand; RetL1; nerve cell; renal failure; nephritis; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis: infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cranial nerve injury; spinal cord injury; Down's syndrome; crerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W37460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting entire growth and improving survival of injured cells, especially renation
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Cate RL, Hession C,
WPI; 98-018431/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
W09744356-A2.
                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 dsss1svapwcdcsnsgndleeclkflnffkdntclknaiga 339
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Score 701; DB 28;
Pred. No. 6.25e-55;
87; Mismatches 95;
                                                                        Length 464;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Mon Mar 8 14:16:14 1999; MasPar time 21.09 Seconds 710.686 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence:

>US-08-866-354-38 (1-400) from US08866354.pep 3033 1 MVRPINPRPIPPVVIMLLLL......PWVPSLESCTLPLILLLSIW 400

Scoring table:

PAM 150 Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir58 1:pir1.2:pir2 3:pir3 4:pir4

Statistics: Mean 45.680; Variance 83.673; scale 0.546

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 4 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
2356 1126 113 113 113 113 113 110 100 100 100 100	Score
7 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Query
397 117 345 1015 1015 1313 1313 1309 496 497 497 497 497 497 497 497 497 497 497	Length
	BB
JE0082 SS2612 XYEC02 A55133 JC5062 JC2038 JC2038 JC2038 SS3484 A69691 XYEBOT XY	ij
GPI-linked receptor - probable membrane pro adaptive response reg gas1 homolog - human transmembrane tyrosin phogrin - human peptidyl-dipeptidase gas1 protein - mouse peptidyl-dipeptidase ATP-dependent DNA hel adaptive response reg protein - human pa macrophage inflammato activin type I recept fibrillin 2 protein - DNA-binding protein - ADR11 2 protein - soy prostaglandin-endoper protein-tyrosine kina pyoverdine synthetase growth-regulated prot secretin - mouse	Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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S48938	S27768	7355	78	I38859	A56558	E71075	D32252	S20455	S71348	A64454	A45493	JH0717	S44250	A27079	VGN2PD	A48346	S69198	G64783	S68257	146083	146199
prot	RNA-directed DNA poly	phosphate transport s	cyclooxygenase 1 – ra	m	acid r	probable proton gluta			Rieske iron sulfur pr	hypothetical protein	phospholipase C-beta	guanylate cyclase (EC	integrin alpha-5 chai			9	prostaglandin G/H syn	ylbF protein - Escher	phospholipase C (EC 3	erythropoietin precur	erythropoietin - dog
Ė	6.11e+00	4.57e+00	4	4.57e+00	4.57e+00	6.11e+00	3.41e+00	<u>.</u>	4.57e+00	6.11e+00	1.88e+00	1.39e+00	1.39e+00			2.54e+00	1.88e+00	1.39e+00	2.54e+00	1.39e+00	1.39e+00

ALIGNMENTS

PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248	Qу 189
IRCORHICLAQIRSFFEKAAESHAQGILLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245	Db 186
YELDVSPYEDTVTSKPWKNNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACK; '	Qy 129
YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEATYT	Db 126
SSISTPLPSBEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRANGUSA	Qу 69
SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHTAT.ST	Db 66
PLPPVVLMLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYIHH.1801	Qy 9
PRPPLLMILLIVISLW-LPIGAGNSLATENREVNSCTQARKKCEANPACKAAYQHIGSCT 4.5	Db 7
Matches 306; Conservative 53; Mismatches 31; Indels 3; Gaps	Matches
	Query Ma
predicted #length 397 #molecular-weight 44307 #checksum 2962	SUMMARY
#region nydrophobic\ 306 #binding_site carbohydrate (Asn) (covalent) #statur	92,145,306
#domain	1-25
glycoprotein	FEATURE
#Cross-relerences DDBJ:ABUU8833; NID:g2627159; PID:g2627160	COMMENT #CI
	##Te
#molecule_type mRNA	##molec
	# 27000
Molecular cloning and expression analysis of GFRalpha.	#title
	#journal
JE0082	REFERENCE
	ACCESSIONS
21-May-1998 #sequence_revision 29-May-1998 #text_change	DATE
NAMES GFRalpha-3	'n
JE0082 #type complete	TITLE
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Best Local
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                                                                                                                                                                              #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession C64991
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                                                                                            ##residues 1-354 ##label BLAT ##cross-references GB:AE000310; GB:U00096; NID:g2367131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 NTTVALSCTCRGSGNLQDECEQLERSESQNPCLVEAIAAKMRFHRQLESQDWADSTESVV 365
                                                                                                                                        ##molecule_type DNA
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                                                            ##experimental_source strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 4.2%;
Local Similarity 41.7%;
nes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Favello, T. submitted to the EMBL Data Library, June 1994. The sequence of S. cerevisiae cosmid L5018.
Nakabeppu, Y.; Kondo,
Sekiguchi, M.
                                                                                                                                                                                                                                                                                   Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                       C64991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptive response regulatory protein - Escherichia coli
methylated-DNA--protein-cysteine S-methyltransferase (EC
2.1.1.63) ada; methylphosphotriester-DNA methyltransferase
#formal_name Escherichia coli
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#formal_name Saccharomyces cerevisiae
05-May-1995 #sequence_revision 19-Oct-1995 #text_change
12-Dec-1997
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                                                                                                                                                             nucleic acid sequence not shown; translation not shown
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Pred. No. 4.51e-05;
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                    Η.;
                    Kawabata,
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                  Iwanaga,
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#title The intracellular signal for induction alkylating agents in e. coli.
#cross-references MUID:86189944
#status
#status
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Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6297-6301

Regulatory mechanisms for induction of synthesis of repair

enzymes in response to alkylating agents: Ada protein act

as a transcriptional regulator.

#cross-references MUID:86313568

#accession 141114
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M.D.; Lindahl, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
#title Active site and complete sequence of the suicidal
methyltransferase that counters alkylation mutagenesis:
#cross-references MID:85190562
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#title Purification and structure of the intact Ada regulator;
protein of Escherichia coli K12, O(6)-methylguanine-DNA
methyltransferase.
#cross-references MUID:85207761
#accession A22630
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##cross-references GB:M10315; NID:g145190;
##experimental_source strain B/r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-29 ##label RE2
##cross-references GB:M13155; NID:g145198; PID:g145199
# cross-references GB:M13155; NID:g145199
# cross-references GB:M13155; NID:g145198; NID:g145199
# cross-references GB:M15199
# cross-references 
                                             32
h 3.8%;
Similarity 31.1%;
23; Conservative
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                                                                                                                                                                                                                                                                           #domain methylated-DNA--protein-cysteine
S-methyltransferase homology #label MGT
#length 354 #molecular-weight 39323 #checksur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA binding; DNA repair; methyltransferase; transcript...
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                                                                                                                                                                                                                                                                                                                                                                                                  #domain methylphosphotriester-DNA methyltransferor-
homology #label MPT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I.; Sedgwick, B.; Kilpatrick, M.W.; McCarthy, T.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translated from GB/EMBL/DDBJ
                                                                                                              Score 116; DB 1;
Pred. No. 1.53e-03
17; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g145191
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Mar 8 14:17:48 1999;

MasPar time 14.56 Seconds 737.504 Million cell updates/sec

Tabular output not generated.

Run on:

Description: Perfect Score: >US-08-866-354-38 (1-400) from US08866354.pep 3033

Sequence: 1 MVRPLNPRPLPPVVLMLLLL......PWVPSLFSCTLPLILLLSLW 400

Scoring table: PAM 150 Gap 11

Searched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 1:swissprot

Statistics: Mean 47.118; Variance 74.608; scale 0.632

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		1 750 2 746 3 707 4 701 5 681 6 674 8 116 9 113 10 113 11 113 11 113 11 108 11 108	Result No. Score
		33333334 33333344 3	% Query Match
1004	1001 1013 352 520 107	465 466 4664 4664 4668 4668 1313 1313 1313 4966	Length
			BB
PTPX_RAT DNBI_BFDV	PTPX_MOUSE PTPX_MACNE ADA_SALTY VL2_HPV19 MI2A_HUMAN SCHD BARTT	NRTR_CHICK SONR_CHICK NRTR_MOUSE NRTR_HUMAN GDNR_MOUSE GDNR_RAT GDNR_HUMAN ADA_ECOLI A	ID
PROTEIN-TYROSINE PHOSP DNA-BINDING PROTEIN (A		NEURTURIN RECEPTOR ALP GDNF RECEPTOR ALP NEURTURIN RECEPTOR ALP NEURTURIN RECEPTOR ALP NEURTURIN RECEPTOR ALP NEURTURIN RECEPTOR ALPHA PR GDNF RECEPTOR ALPHA PR GDNF RECEPTOR ALPHA PR ADA REGULATORY PROTEIN GROWTH-ARREST-SPECIFIC PROTEIN-TYROSINE PHOSP ANGIOTENSIN-CONVERTING GROWTH-ARREST-SPECIFIC ANGIOTENSIN-CONVERTING ANGIOTENSIN-CONVERTING ANGIOTENSIN-CONVERTING ANGIOTENSIN-CONVERTING ANGIOTENSIN-CONVERTING	Description
1.08e-01 2.15e-01	6.09e+03 8.79e-03 2.61e-02 1.82e-02 5.34e-02	3.47e-155 3.72e-154 3.97e-144 1.37e-142 1.07e-136 1.13e-137 2.00e-04 6.38e-04 6.38e-04 6.38e-04 6.38e-04 6.38e-04 6.38e-04 6.38e-04 6.38e-04	Pred. No.

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FGD1_MOUSE	PSTA_MYCPN	SFUB_SERMA	KIR2_HUMAN	SRPX_HUMAN	PQQC_ACICA	GCP2_HUMAN	CC12_SCHPO	CYGD_CANFA	CYGD_HUMAN	ITA5_MOUSE	ITA5_HUMAN	HEXA_ANOGA	VGLF_PHODV	PHZF_PSEAR	YLBF_ECOLI	EPO_CANFA	SECR_MOUSE	GRO_CRIGR	FBN2_HUMAN	TBG_ENTHI	DHEZ MOUSE
PUTATIVE RHO/RAC GUANI	PHOSPHATE TRANSPORT SY	IRON(III)-TRANSPORT SY	SERINE/THREONINE-PROTE	SUSHI REPEAT-CONTAININ	COENZYME PQQ SYNTHESIS	GRANULOCYTE CHEMOTACTI	CELL DIVISION CONTROL	RETINAL GUANYLYL CYCLA	RETINAL GUANYLYL CYCLA	FIBRONECTIN RECEPTOR A	FIBRONECTIN RECEPTOR A	HEXAMERIN 1.1 PRECURSO	FUSION GLYCOPROTEIN PR	PROBABLE PHOSPHO-2-DEH	HYPOTHETICAL 29.6 KD P	ERYTHROPOIETIN PRECURS	SECRETIN PRECURSOR.	GROWTH REGULATED PROTE	FIBRILLIN 2 PRECURSOR.	TUBULIN GAMMA CHAIN.	ESTRADIOL I/ BETA-DERY
1.60e+00	1.60e+00	2.22e+00	1.60e+00	1.16e+00	1.16e+00	1.60e+00	5.96e-01	4.26e-01	4.26e-01	4.26e-01	8.31e-01	4.26e-01	8.31e-01	4.26e-03	4.26e-01	4.26e-01	8.31e-01	5.96e-01	3.03e-01	1.53e-01	1.536-01

ALIGNMENTS

Query Match 24.7%; Best Local Similarity 35.5%; Matches 125; Conservative	RESULT ID RRTR_CHICK AC O13157; DT O1-NOV-1997 (REL. 35, CREATED) DT O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) DT O1-NOV-1997 (REL. 36, LAST SEQUENCE UPDATE) DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) DT O1-NOV-1997 (REL. 36, LAST SEQUENCE UPDATE) DT O1-NOV-1997 (REL. 36, LAST SEQUENCE UPDATE) DT O1-NOV-1998 (REL. 36, LAST SEQUENCE UPDATE) DT NECRTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (N RECEPTOR BETA) (GDNER-BETA). OS GALLIS (GALLUS (CHICKEN). OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPOD OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPOD OC EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPOD OC CALLIFORMES. RN SEQUENCE FROM N.A. ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES RA SUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THO RA SEQUENCE 387:721-724 (1997). CC -1-FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE CO -1-FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE CO -1-FUNCTION: RECEPTOR FOR NEURTURIN OF THE RET TYRO CC -1-FUNCTION: RECEPTOR FOR NEURTURIN OF THE RET TYRO CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE RET TYRO CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE RET TYRO CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE MEMBRANE CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE MEMBRANE CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE RET TYRO CC -1-SUBCELULLAR LOCATION AND ACTIVATION OF THE MEMBRANE TO MEMBRANE TO MEMBRANE R	
Score 750; DB 1; Length 465; Pred. No. 3.47e-155; 93; Mismatches 109; Indels 25; Gapts :	D; PRT; 465 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) HA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (GDNF BETA).). ORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; PINON L.G.P., HORTON A., THOMPSON J., RU M., BUCHMAN V.L., DAVIES A.M.; 7). FOR NEURTURIN. MEDIATES THE NRTN-INDUCED N AND ACTIVATION OF THE RET RECEPTOR. ALSO ANAITY). ON: ATTACHED TO THE MEMBRANE BY A GPT-ANTHAL. POTENTIAL. POTENTIAL	

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Best Local
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CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                   DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) ('NEUROTROPHIC FACTOR RECEPTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                       BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M., NATURE 387:721-724 (1997)

-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNR_CHICK O13156;
                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
              120
                                                                                                                                                                                                                                                                                                        RECEPTOR;
                                                                                                                                                                                                                                                                                                                                        - I - SUBCELLULAR LOCATION: SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERA1 OR GDNFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
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                                    73
                                                           61
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                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS
L; U90541; G2213803;
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET (BY SIMILARITY).
                                                                               MILLL-LPPSPLPLAAG-DPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCTSSIS 72
EDSPYEPVNSRLSDIFRLAPIVSVEPVLSKGNNCLDAAKACNLNDTCKRFRSAYITPCTS 179
                                                                                                     LALLYLALPLADVLLSAEVSGLPGGDRL-D-CVKASDQCLKEQSCSTKYRTLRQCVAGKE 60
                                 TPLPSEEP-SVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNYEL
                                                 SNFSRATGLEAKDECKSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDMTPNYVDASTTSITISPWCSCKGSGNLEEECEKFLRDFTENPCLRNAIQA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CS---GP--HCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSKEISATEHCSRRKCHKALROFFDNVPSEYTYRLLFCSC--KDQACAEPRRQTIVPFCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEDKEKPNCLDLRNVCRADHLCRSRLADFHANCQASFQSLTSCPGDNYQACLGSYTGLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPVA-PNCLELRRLCFSDPLCRSRLVDFQTHCHP-MDILGTCATEQSR-CLRAYLGLIG
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                                                                                                                              l Similarity
127; Conser
                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN;
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163
163
346
405
430
469
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431
                                                                                                                              Conservative
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                                                                                                                                                                    368
62
163
163
446
430
52043
                                                                                                                                         24.68;
                                                                                                                                                                                                                                                                     27
430
469
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                                                                                                                                                                                                                                                                                                      GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                             TO THE GDNFR FAMILY.
                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                   ATTACHED TO THE MEMBRANE
                                                                                                                           Score 746; DB 1; L
Pred. No. 3.72e-154;
69; Mismatches 132;
                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR
07: C8D241C9
                                                                                                                                                                                                                                              (POTENTIAL).
POLY-THR.
                                                                                                                                                                                                                                                                   HYDROPHOBIC,
                                                                                                                                                                                                                                                                                 GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                    POTENTIAL.
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CRC32;
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                                                                                                                                                                                                                                                                                                      SIGNAL.
                                                                                                                                                  Length 469
                                                                                                                             Indels 18;
                                                                                                                                                                                                                                                                                                                                                  BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELATED
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                                                                                                                            Gaps
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Matches 11
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CARBOHYD
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LIPID
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA;
EUTHERIA; R
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MEDLINE; 97325791.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEI

HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B.,

JOHNSON E.M. JR., MILBRANDT J.;

NEURON 18:793-802(1997).
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPH
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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01-NOV-1997
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96 KRGMKKELQCLQIYWSIHLGLTEGE-EFYEASPYEPVTSRLSDIFRLASIFSGTGA-WAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL, AND DORSAL ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
TISSUE SPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND IN THE ADRENAL.
                                                                                  CLQARRKCQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLICC:
                                                                                                                                           CVRANELCAAESNCSSRYRTLRQCLAG-RDR-NTMLAN--KECQAALEVLQESPI.NTMTHT. | : : : : | | : | ::|:| | | : | : | | : | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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llarity 36.2%;
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413
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                                                                                                                                                                                                                                           Score 707; DB 1; L
Pred. No. 3.97e-144;
83; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROPHOBIC,
(POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

GPI-ANCHOR (POTENTIAL).

MISSING (IN SHORT FORM)
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RECEPTOR 2) (GDNF
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D.B., POPESCU
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                                                                                                                                                                                                                                                                                                               Length 463
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ONF RECEPTOR BETA)
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T11641	T01040	T08768	T01039	T01050	T01048	T65667	T65718	T65730	Q33639	T65766	T96631	T86172	V04102	V19709	T63575	Q26683	T47511	T68682	Q55246	Q27097	Q51746	Q34050	Q33849	T33007	T60965	T78597	Q27100	Q27094	T65659	T65721	020685
Murine osteogenic pro	Mouse B7-1 exons 1, 2	lyca	e B7-1 exons 1,	B7 - 1	7-1 exons 1,	orphic repe		W	atellite s	at sequence fr	ncoding rat cy	nucleo	oryz	evulinic aci	cken beta-act	dopamine	н	annamei gen	Grapevine ribosomal c	ile x diagno	eotide	satellite	tellite se	RY-	in-	in-accumula	x diagnos	agnosti	ymorphic rep	epeat sequen	PKS 741 insert contq.
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ALIGNMENTS

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PN W09744356-A2.

PD 27-NOV-1997; U07726.

PF 07-MAY-1997; U07726.

PR 10-APR-1997; US-017427.

PR 10-APR-1996; US-013000.

PR 10-APR-1996; US-01359.

PR 08-MAY-1996; US-021859.

PR 16-JUL-1996; US-021859.

PR 16-JUL-1996; US-021859.

PR 1810J) BIOGEN INC.

PR 1810J) BIOGEN INC.

PR WPI; 98-018431/02.

PR -PSDB; W37460.

PT vectors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr reve cells

PT revetors, transformed cells and antibodies, used for promoting cell pr reve cells

PT revetors, transformed cells and antibodies, used for promoting cell pr revetors, transformed cells and antibodies, used for promoting cell pr revetors, transformed cells and antibodies, used for promoting cell pr revetors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr vectors, transformed cells and antibodies, used for promoting cell pr vectors, used for
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C V00248;

Y 21-MAY-1998 (first entry)

121-MAY-1998 (first entry)

E Human Ret ligand retL2 cDNA.

W Ret ligand; RetL; RetL2; receptor; signal transduction; human; two cell growth; renal cell; nerve cell; renal failure; nephritis; w cingy transplant; toxic injury; hypoxic injury;

W neurodegeneration; motor neurone disease; multiple sclerosis; meurodegeneration; menor eurone disease; multiple sclerosis; w infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; w cranlal nerve injury; spinal cord injury; Down's syndrome; w cranlal nerve injury; spinal cord injury; Down's syndrome; w cranlal palsy; Lyme disease; muscular dystrophy;

W myasthenia gravis; tumour; therapy; ss.

S Homo saplens.
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SQ Sequence 1888 BP; 399 A; 593 C; 536 G; 360 T;
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larity 89.8%;
Conservative
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Pred. No. 0.00e+00;
0; Mismatches 148;
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
16-ETH ) GENENTECH INC.
K1611 RD, MOOFE MM, ROSENTHAL A, RY
WPI; 97-470819/43.
Isolated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorcexample 1; Page 61; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                             Human EST-derived sequence y170a10.rl. Glial cell derived neurotrophic factor receptor alpha; GDNF; human; kidney disease; glomerulonephritis; therap expressed sequence tag; EST; ss.
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Best Local S
Matches 39
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                                                                                                          Human EST-derived sequence ye83h05.rl.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                  1444
                                                                                                                                                                                                                                                                                                                                                                                                                                               1384
18-SEP-1997.
13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
                                                              Homo sapiens.
WO9733912-A2.
                                                                                           expressed sequence tag; ss.
                                                                                                                                                          T84978;
27-APR-1998
                                                                                                                                                                                       T84978 standard; DNA;
                                                                                                                                                                                                                                                                                      421
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                                                                                                                                                                                                                                                                      gggtcttnatgttggcatgattgggtttgacat 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcatgctcttctgctcctgccaagaccaggcgtgcgctgagcgcgcggggcaaaaccatcc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcaagtgccacaaggccctgcgccagttcttcgaccgggtgcccagcgagtacacctacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCCACCGAACGCTGCAACCGCC 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gctcctcctacatctccatctgcaaccgcgagatctcgcccaccgagcgctgcaaccgcc 120
                                                                                                                                                                                                                                                                                                                                                                                                    gccggactgaccacctgtgtcggtcccggctngccgactttccatgccaatttgttcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgcccagctgctcctatgaggacaaggagaaagcccaactgcctggacctgcgtggcgtgt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGCTCTTCTGCTCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccttcctaccagacgggtcaccaggctgccctngcggacaatttaccagggcgtgtcttg
                                                                                                                                                                                                                                                                                                                                                                               GTCGTACAGACCACCTGTGCCGGTCCCGACTGGCAGA-TTTCCACGCCAACT-GT-CGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
396; Conse
                                                                                                                                                          (first entry)
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larity 87.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                    -GCGGACAACT-ACCAGG-CATGTCT-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DRA sequence comprises a human EST-derived sequence designated ye83h05.rl. It can be used to identify glial cell derived neurotrophic factor receptor (GDNFR) sequences, including human cyaliants. Also suitable as probes for GDNFR sequences are another human EST-derived sequence designated y770al0.rl (see T84979), and fragments of these EST-derived sequences (see T84980-81) or proteins encoded by them. The invention relates to novel uses of GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, grantifying molecules homologous to GDNFR alpha, and claimed conditions, particularly kidney disease associated with conditions, particularly kidney disease associated with GTRansgenic and knockout animals are also claimed.

Sequence 351 BP; 77 A; 117 C; 96 G; 57 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
Klein RD, Moore MW, Rosenthal A, Ryan
WPI: 97-470819/43.
                                                                                                                                                                                      T95297 standard; cDNA; 213
T95297;
01-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 1378
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                                                                                 Huntington's disease; gene therapy; ss.
                                                                                                                 Rat glial cell line-derived neurotrophic factor receptor cDNA. Rat; glial cell line-derived neurotrophic factor; GDNF; receptor: treatment; dopaminergic nerve cell disorder; Parkinson's disease; alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
                                                                Rattus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTTCGCTCCTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGAACGCTGCA 1257
                                                                                                                                                                                                                                                                                                                                                                 CCTACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAA 1'47'
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l Similarity 89.08;
276; Conservative
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                                                                                                 glaucoma;
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Pred. No. 1.90e-156;
0; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and PT claim 17; Pages 96-98; 196pp; English.

CC The present sequence encodes the rat glial cell line-derived companiergic nerve cell disorders, e.g. Parkinson's and Alzheimer's CC disease or amyotrophic lateral sclerosis, complications of diabetes CC and Huntington's disease and (optionally in combination with GDNF) CC gliaucoma, retinal degeneration and hearing loss caused by injury to cinner ear sensory neurons. The receptor can also be used to block CC unwanted GDNF activity, analyse GDNF related molecules and cells, preferably transfected ex vivo, can be used to block CC stabilise GDNF in pharmaceutical formulations. Receptor expressing CC cells, preferably transfected ex vivo, can be used to identify by CC implantation, and the use of the receptor CDNA in gene therapy is CC also contemplated. Probes based on the CDNA can be used to identify cC GDNF responsive cells and tissues, e.g. to identify patients who CC would benefit from GDNF therapy, and abnormalities in receptor CC antibodies, oligonucleotides derived from the CDNA. Anti-receptor CC antibodies, oligonucleotides derived from the CDNA and animal complex with the CDNA can be used to study the biological function of GDNF, knockout transgenic animals can be complex that mediates/enhances signal transduction by GDNF, i.e. CC complex that mediates/enhances signal transduction by GDNF, i.e. CC increasing dopamine uptake in dopaminergic cells.

Sequence 2138 BP; 494 A; 593 C; 584 G; 467 T;
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Best Local
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30-OCT-1997; U06281.
15-APR-1997; US-837199.
14-APR-1996; US-015907.
09-MAY-1996; US-017221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC. Fox GM, Jing S, Wen D; WPI; 97-535836/49.
                                                                                                                                                                                                                                                                                                  679
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                                                                                                                                                                                                                                                                                                                                                                                                          950
                                                                                                                                                                                                                                                                                                                                                                                                                               ccgctgcbagcggggcatgaagaagaagaattgtctgcgtatctactggagcatgta 621
caagcacagctacgggatgctcttctgctcctgccgggacatcgcctgcaccgagcggcg
                                                                                                            CTGCAAGAAGCTTCGCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCCACCGA
                                                                                                                                  GGTCAGTACCAAAAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAATGACAA
                                                                                                                                                                                                           acacatttccaaagggaacaactgcctggacgcaaggccaaggcctgcaacctggacgacac
                                                                                                                                                                                                                                                            GCGCCTCTCGGACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGC
                                                                                                                                                                                                                                                                                 ACGCTGCAACCGCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAG
                                                          ggtctgcaaccgccgtaagtgccacaaggccctcaggcagttcttcgacaaggttccggc
                                                                                                                                                                                                                                                                                                                                    TCTGGGGCTGACAGAGGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTC
                                                                                                                                                                                                                                                                                                                                                           ccagagcctg-cag--ggaaatgacctcctggaagattccccgtatgagccggtttaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213; DB 38;
Pred. No. 6.89e-132;
0; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2138;
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                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
nerve cells
Claim 1; Page 46-49; 113pp; English.
Claim 1; Page 46-49; 113pp; English.
This sequence comprises rat retL1 cDNA (deposited as ATCC 98047)
that codes for the Ret ligand RetL1 (see W37457), a key component
of the Ret signalling pathway. It consists of the insert of clone
#230-5A-86-17 that was isolated from a rat embryonic kidney CDNA
                                                                                                                                                                  New nucleic acid encoding ret receptor ligands and related professervectors, transformed cells and antibodies, used for promoting encountry and improving survival of injured cells, especially renaises
                                                                                                                                                                                                                                                                  (BIOJ ) BIOGEN INC.
Cate RI, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
P-PSDB; w37457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V00245 standard; cDNA; 3616 BP.
V00245;
V00245;
21-MAY-1998 (first entry)
Rat Ret ligand retL1 CDNA.
Ret ligand; RetL; receptor; signal transduction; rat;
cell growth; renal cell; nerve cell; renal failure; nephriti
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Best Local Similarity 65.3%;
Matches 583; Conservative
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                            CC embryos was generated in a cytomegalovirus-based vector. CNA
CC clones were transfected into COS 7 cells and expression of
CC putative GDNF receptors was detected by binding of iodinated GDNF.
CC A single positive pool was obtained, from which the cDNA clone was
CC isolated. An expression vector containing the cDNA can be used to
CC produce GDNFR alpha in transformed host cells. The invention
CC relates to novel uses of GDNF and its receptor. In particular, it
CC relates to notive rat GDNFR alpha (see W27327), its variants and
CC soluble derivatives (extracellular domain), chimeric GDNFR alpha
CC and nantibodies which bind to the GDNFR alpha, including agonist
CC and neutralising antibodies, as well as various uses for these
CC molecules. It also relates to assay systems for detecting ligands
CC molecules. It also relates to assay systems for detecting ligands
CC molecules. It also relates to assay systems for detecting ligands
CC to GDNFR alpha, systems for studying the physiological role of
CC GDNFR diagnostic techniques for identifying GDNF-related conditions,
CC therapeutic techniques (claimed) for the treatment of GDNF-related
CC and GDNFR alpha-related conditions, particularly kidney disease
CC associated with glomerulonephritis and enteric nervous system
CC related disorders. Transgenic and knockout animals are also
                                                                                                                                                                                                                                                                                                                                                                                                                                  A (GETH) GENEWIECH INC.

NA KLein RD, Moore MW, Rosenthal A, Ryan AM;

NR WPI; 97-470819/43.

NR WPI; 97-470819/43.

P-PSDB; W27327.

TISOlated glial cell derived neurotrophic factor receptor alpha disorders particularly enteric nervous system or kidney disorders of starticularly enteric nervous system or kidney disorders of specific to disorders, particularly enteric nervous system or kidney disorders of specific to disorders of the claim 23; Page 74-77; 100pp; English.

Claim 23; Page 74-77; 100pp; English cell derived neurotrophic factor receptor alpha (GDNFR alpha) (see W27327), a novel correction that is a ligand-binding component of the receptor system for GDNF. It was isolated by expression cloning.

C A cDNA library obtained from ventral middlersin tissue of E14 rat
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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CI The present sequence encodes the human glial cell line-derived CC neurotrophic factor (GDNF) receptor, which can be used to treat CC dopaminergic nerve cell disorders, e.g. warkinson's and Alzhelmer's CC disease or amyotrophic lateral sclerosis, complications of diabetes CC and Huntington's disease and (optionally in combination with GDNF) CC glaucoma, rethal degeneration and hearing loss caused by injury to cinner ear sensory neurons. The receptor can also be used to block CC unwanted GDNF activity, analyse GDNF related molecules and cells, preferably transfected ex vivo, can be used to block CC implantation, and the use of the receptor cDNA in gene therapy is CC also contemplated. Probes based on the CDNA can be used to identify patients with CC would benefit from GDNF therapy, and abnormalities in receptor CC expression, and to isolate molecules that form a complex with the CDNA or are homologous/cross-reactive with the CDNA. Anti-receptor antibodies, oligonucleotides derived from the cDNA and animals can be used to detect GDNF dependent neurons or processes and the antibody Cc can be used in immunoassays for the receptor. The receptor binds CC can be used in immunoassays for the receptor. The receptor binds CC complex that mediates/enhances signal transduction by GDNF, i.e. CC increasing dopamine uptake in dopaminergic cells.

Sequence 2568 BP; 631 A; 662 C; 625 G; 607 T;
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30-OCT-1997; U06281.
15-APR-1997; U5-837199.
14-APR-1996; US-837199.
22-APR-1996; US-015907.
09-MAY-1996; US-017221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treat dopaminergic nerve cell disorders, e.g. Parkinson's and
Alzheimer's disease
Claim 17; Pages 91-93; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
Fox GM, Jing S, Wen D;
WPI; 97-535836/49.
P-PSDB; W353333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glial cell line derived neurotrophic factor receptor - useful
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/*tag= a
/product= GDNF_receptor
Length 2568;
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Matches Query Match Best Local 571; h 9.5%; Similarity 65.5%; 571; Conservative Score 210; DB 38; Pred. No. 1.16e-129; 0; Mismatches 289; Mismatches 289; Indels 12: 1311111

Ş Ş 밁 용 밁 Ş 밁 Ş Ş 밁 Ş 밁 1070 1010 917 800 990 740 tgtctgcaaccgccgcaagtgccacaaggccctccggcagttctttgacaaggtcccggc ggccaaggatgagtgccgcagcgccatggaggccctgaagcagaagtcgctctachacha ccagagcctg-cag--ggaaatgatctgctggaggattccccatatgaaccagttaacag ccgctgcaagcggggtatgaagaaggaagaactgcctgcgcatttactggaacatqlo GGCCAATAAGGAGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAAGCCCACTGTATGACT:; GCGCCTCTCGGACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGC TCTGGGGCTGACAGAGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTC CCGCTGCAAGCGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCATCCA 1. 976 9.J.ç 1069 3

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This DNA sequence comprises a fragment of a human EST-derived sequence designated ye83h05.rl (see T8478). It can be used as sequence designated ye83h05.rl (see T8478). It can be used as probe to identify glial cell derived neurotrophic factor receptor (GDNF) sequences, including human variants. The invention relates to novel uses of GDNF and its receptor. In particular, it relates to rat GDNFR alpha (see w27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNF, diagnostic techniques for identifying molecules homologous to GDNFR alpha, methods for identifying molecules homologous to GDNFR alpha, and claimed methods for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with Transgenic and knockout animals are also claimed.
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Klein RD, Moore MW, Rosenthal A, Ryan AM;

KPI; 97-470819/43:
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Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
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14-MAR-1996; US-615902.
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184980 standard;
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                                                                                                    This DNA sequence comprises a fragment of a human EST-derived CC sequence designated y170al0.rl (see T8479). It can be used as ca probe to identify glial cell derived neurotrophic factor receptor CC (GDNFR) sequences, including human variants. The invention relates to novel uses of GDNF and its receptor. In particular, it relates ct or at GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which cc bind to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also crelates to assay systems for detecting ligands to GDNFR alpha, correct dentifying molecules homologous to GDNF alpha, and claimed conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system related disproduct. CC conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system related disproduct. Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
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Best Local
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WPI; 97-470819/43.
Isolated glial cell derived neurotrophic factor receptor alpha
useful to develop products to diagnose and treat associated
disorders, particularly enteric nervous system or kidney disord
Example 1; Page 61; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human EST-derived sequence y170a10.rl fragment.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
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14-MAR-1996; US-615902.
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14-MAR-1996;
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WO9733912-A2.
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187; Conser
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ilarity 94.0%;
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Pred. No. 8
0; Mismat
                                           Score 175; DB 37;
Pred. No. 8.03e-104;
0; Mismatches 12;
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                                                           This sequence comprises a partial CDNA for human Ret ligand (RetL) created from a human embryonic kidney cDNA library using rat retLl cDNA (see v00245) as probe. A full-length sequence (see v00247) for human retLl cDNA has also been obtained, as well as containing retLl DNA and prokaryotic or eukaryotic host cells containing retLl DNA and prokaryotic or eukaryotic host cells transformed or transfected with these vectors are claimed, as well as a method for production of RetLl, its soluble variants and custom proteins with a toxin, imageable compound or radionuclide. RetLl, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, perficularly kidney or neural tissue. Typical applications are in crenal failure, nephritis, kidney transplants, toxic or hypoxic myelopathy associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and cut. to Ret-expressing cells, especially tumours.
   Matches
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07-MAY 1997; U07726
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-017427.
07-JUN-1996; US-019300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebral palsy; Lyme disea; myasthenia gravis; tumour; Homo sapiens
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Ret ligand; RetL; RetLl; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; cerebral palsy; Lyme disease; muscular dystrophy;
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Claim 1; Page 58-60; 113pp;
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                  Similarity
 7.5%;
larity 66.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy;
Score 166; DB 39;
Pred. No. 3.22e-97;
0; Mismatches 200
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     200;
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                                                           27-NOV-1997.
07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                      Human Ret ligand retil cona.

Ret ligand; Reti; Retil; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                         (BIOJ ) BIOGEN INC. Cate RL, Hession C, WPI; 98-018431/02.
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21-MAY-1998 (first entry)
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V00247 standard; cDNA; 1682
           P-PSDB; W37459
                                                                                                                                           W09744356-A2.
                                                                                                                                                                                           Homo sapiens
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Retti (see W37459), a key component of the Ret signaling pathway. CC cDNA using primers based on a partial human retti cDNA (see V00246). Rat retti and mouse and human retti cDNA (see V00246). Rat retti and mouse and human retti cDNA (see CC V00246). Rat retti and mouse and human retti cDNA (see CC containing retti DNA and prokaryotic or extil cDNA. Vectors containing retti DNA and prokaryotic or exaryotic host cells transformed or transfected with these vectors are claimed, as well cas a method for production of Retti, its soluble variants and component of new tissue and survival of damaged tissue, potionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, containing kidney or neural tissue. Typical applications are in cranal failure, nephritis, kidney transplants, toxic or hypoxic conjury, neurodegeneration, motor neurone disease, multiple called the protest of sectors is bacterial, viral or prion infections (e.g. meningitis, conjury associated with HIV or Creutzfeldt-Jakob disease), conjury associated with HIV or Creutzfeldt-Jakob disease), see Conjury and cerebral palsy, or conditions involving the componental disorders such as Down's syndrome and cerebral palsy, or conditions involving the componental disorders. Fusion proteins are used to deliver toxins cetc. to Ret-expressing cells, especially tumours.
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Claim 1; Page 62-64; 113pp;
1673
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    vectors, transform
growth and improving

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les 420; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGAAGCTTCGCTCCTCTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGAACG 1252
                                 gtgcttgaaattttttgaatttcttcaaggacaatacatgtcttaaaaattgcaattcaagc 1133
                                                                                                                                             cctcgcctactcggggcttattggcacagtcatgacccccaactacatagactccagtag
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                                                                                                            CACGGGCATCGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGA
                                                                                                                                                                                                                           GGGCTCCTATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCC 1612
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Pred. No. 3.22e-97;
0; Mismatches 200; Indels 0
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injured cells, especially renal or
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Example 1; Page 60-61; 100pp; English.

This cDNA sequence comprises the 3' end of mouse full-length glal cell derived neurotrophic factor receptor alpha (GDNFR alpha; CSC 91sal cell derived neurotrophic factor receptor alpha (GDNFR alpha; CSC 91sal cell derived neurotrophic factor receptor alpha (GDNFR alpha; CSC 10se 26 was isolated from a mouse cDNA library using rat GDNFR alpha cDNA (see T84975) as probe. The invention relates to notice rat GDNFR alpha (see T84975), its variants and soluble rat GDNFR alpha (see W27327), its variants and soluble to native rat GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimneric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antibodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNF diagnostic techniques for identifying GDNF-related conditions, methods for identifying molecules homologous to GDNFR alpha, end alpha, end of the related conditions, particularly kidney discussional conditions, particularly kidney discussional discussions associated with glomerulonephritis and enteric nervous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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T84977
T84977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse GDNFR alpha clone 26 3' end.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                        1380
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W09733912-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1733 CTTTGGTAATGGCACAGATGTGAACATGT 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH Klein RD, Moore M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997; U04363.
14-MAR-1996; US-618236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-470819/43.
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                                   ccagagtcaaggtctgtcagcaactgtcttaaggagaactacgcagactgcctcctggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCGCATGCTCTTCTGCTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacgggatgctcttctgctcctgccgggacgtcgcctgcaccgagaggcggcgacagact 120
   TATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCCCACGGGC
                                                                                                                                                                                                                                                                                                                                                                        ATCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCGCAGC
                                                                                                                          GCCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATGTCTGGGCTCC
                                                                                                                                                                                                                                                 CTGTGTCGTACAGACCACCTGTGCCGGTCCCGACTGGCAGATTTCCACGCCAACTGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 5.6%;
l Similarity 64.8%;
339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125; DB 37; I
Pred. No. 1.94e-67;
0; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>A</u>
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PN W09200375-A.

PD 09-JAN-1992.

PF 28-JUN-1991; GB-015488.

PR 13-JUL-1990; GB-01085.

PR 13-JUL-1990; GB-010085.

PR 13-JUL-1990; GB-010085.

PR 09-MAY-1991; GB-010085.

PR 13-JUL-1990; GB-011085.

PR 13-JUL-1990; GB-01085.

PR 13-JUL-1990; GB-011085.

PR 13-JUL-1990; GB-01085.

PR 13-JUL-1990; GB-011085.

PR 13-JUL-1990; GB-01085.

PR 13-JUL-199
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S Mus musculus.

N M0920375-A.

09-JAN-1992.
D 99-JAN-1991; G0-014446.
R 18-JUN-1990; GB-014448.
R 13-JUN-1990; GB-01085.
R 09-MAY-1991; GB-010085.

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Best Local Similarity 88.6%;
Matches 62; Conservative
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22-APR-1992 (first entry)
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Pred. No. 4.25e-15;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                        protection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers plsclosure; Column 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dC-dT)n which can be used to detect the repeats, especially for use in e.g paternity or maternity the sequence commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(discontinuous) over 100 repeat blocks were isolated. The inserts from the containing the repeat sequences were isolated. The inserts from the containing the sequence series with a synthetic poly(dC-dA). (discontinuous) over 100 repeat blocks were isolated. The inserts from the containing the formula are shown in T65704-797. This reposit sequence has been determined are shown in T65704-797. This reposit sequence having the formula: (AC)8AG(AC)3AG(AC)2ATCAC(TC)6T.
                                                                                                                                                                            Query Match
Best Local S
Matches 5
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.

US558279-A.

10-DEC-1996.

21-APR-1989; 341562.

21-APR-1989; US-341562.

21-APR-1991; US-75451.

04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting Y chromosomes
Claim 7; Page 122 and Fig 19(1-3); 183pp; English.
The mouse gene equivalent to the human Y-Located gene defined by py53.3 (Q20684), is referred to as Sex-determining Region of the Y-chromosome (Sry) (formerly (mating type box y) Mty).
The mouse Sry is expressed in male genital ridge, at the time that sex determination occurs, and adult testis see also Q20680-81, Q20684-87, Q22530-31, Q22535-36 and Q22560-67.
Seculence 14704 BP; 4259 A; 3237 C; 3099 G; 4103 T;
                                                          2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 15
T65721 standard; DNA; 91 BP
T65721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd19.
Polymorphism; repeat sequence; genetic marker; primer; amplification polymorphism; rehain reaction; paternity; maternity; human; positions, polymerase chain reaction; paternity; maternity; human; positions paralysis; genetic disease; animal; plant; breeding; locus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD
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83
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                                                                                            97-042299/04.
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Similarity 88.6%;
62; Conservative
                                                                                                                                                                               Similarity
59; Conser
                                                                                                                                                                            2.1%;
larity 88.1%;
Conservative
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Pred.
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                                                                                                                                                                               0
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                           No :
                                                                                                                                                                   DB 25,
3.26e-13;
7;
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human: ເຕີ່າ:
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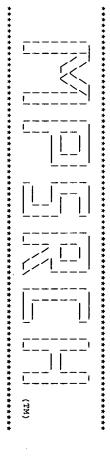
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2195 TACAGAC

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Search completed: Fri Mar 12 10:08:30 1999 Job time: 454 secs.

Stagn AND THE FORM SILL



Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd Unit.

con on : MPsrch_pp protein - protein database search, using Mon Mar 8 14:25:40 1999; MasPar time 16.27 Seconds 457.512 Million cell updates/sec Smith-Waterman algorithm

Tabular output not generated

Title: >US-08-866-354-40

Description: Perfect Score:

Sequence: (1-460) from US08866354.pep
3343
1 MLVFPSHYPDETLRSLASPS......RARLSAALTALPLLMLTLAL

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database: a-geneseq32

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Statistics: Mean 34.963; Variance 141.378; scale 0.247

score greater than or equal and is derived by analysis of Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by the p greater than or equal to the score of the result being derived by analysis of the total score distribution printed,

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Regult No.
3131 1560 1560 1560 1520 1523 1523 1444 1144 777 777 103 99 99 89	Score
201123445667777 20123445667777	% Query Match
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W37460 W35334 W375334 W37457 W27727 W27727 W37459 W37461 W37465 W37466 W37466 W37466 W37466 W37466 W37466 W37467	ID
Human Ret ligand RetL Rat glial cell line-d Rat Ret ligand RetLi. Rat glial cell derive Human glial cell line Human Ret ligand RetL Human Ret ligand RetL Mouse Ret ligand RetL Mouse Ret ligand RetL Human Ret ligand Ret ligand RetL Human Ret l	Description
0.00e+00 1.20e-147 1.20e-147 1.20e-147 1.20e-144 1.94e-141 5.39e-166 4.61e-59 4.61e-59 2.29e-55 4.61e-59 2.29e-55 4.14e+01 1.14e+01 2.26e+01 2.26e+01 5.24e+01	Pred. No.

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ALIGNMENTS

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07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                               nerve cells
Claim 2; Page 69-70; 113pp; English.
Claim 2; Page 69-70; 113pp; English.
This amino acid sequence comprises human Ret ligand (RetL) RetL2;
deduced from a cDNA clone (see V00248) isolated from a human foctor
liver library. Rat and human RetL1, and human and mouse RetL3
sequences (see W37457-59 and W37461-63) are also claimed. Human
RetL2 is 49.1% identical to human RetL1 protein. RetL is a
RetL2 is 49.1% lentical to human RetL1 protein. RetL is a
Rey component of the Ret signalling pathway that specifically
interacts with Ret receptor protein, triggering Ret dimerisation
and/or autophosphorylation of the Ret tyrosine kinase domain
vectors containing retL2 DNA and prokaryotic or eukaryotic host
cells transformed or transfected with these vectors are claimed, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Ret ligand RetL2.

Ret ligand; RetL; RetL2; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                                   New nucleic acid encoding ret receptor ligands and related professions - vectors, transformed cells and antibodies, used for promoting congrowth and improving survival of injured cells, especially results.
                                                                                                                                                                                                                                                                                                                                                                                           (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W37460;
21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens. 
WO9744356-A2.
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  fusion
                      well as a method for
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V00248
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proteins with
production of RetL2, its soluble variants as a toxin, imageable compound or radionuclide.
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RESULT
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Best Local S
Matches 42
                                                                                                                               30-OCT 1997.
15-APR-1997; U06281.
14-APR-1997; US-837199.
22-APR-1996; US-015907.
09-MAY 1996; US-017221.
                                    (AMGE-) AMGEN INC.
FOX GM, Jing S, Wen
WPI: 97-535836/49.
N-PSDB; T95297.
              Glial
                                                                                                                                                                                                                                                                                                                                                    Rat glial cell line-derived neurotrophic factor receptor. Rat; glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; allzheimer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glaucoma; retinal degeneration; hearing loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w35334 standard;
w35334;
01-MAY-1998 (fi
                                                                                                                                                                                                                                                                             Rattus sp. W09740152-A1.
                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 gsnkvikpnsgpsrarpsaaltvisvimiklai 464
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428 GSKKVIKLNSGSSRARLSAALTALPILMLTLAL 460
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              cell
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427; Conser
        line derived
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neurotrophic factor receptor -
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Pred. No. 0.00e+00;
17; Mismatches 9;
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XXEDACE

LT 3 W37457

standard;

Protein;

468

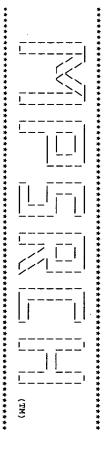
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W37457; 21-MAY-1998 (first entry) Rat Ret ligand RetL1. Ret.ligand; RetL; RetL1; recell growth; renal cell; ne.

receptor; signal transduction; nerve cell; renal failure; nep

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The present sequence is the rat gillal cell line-derived CC neurotrophic factor (GDNR) receptor, which can be used to treat CC dopaminergic nerve cell disorders, e.g. parkinson's and Alzhelmer's CC disease or amyotrophic lateral sclerosis, complications of disbetes CC disease or amyotrophic lateral sclerosis, complications of disbetes CC and Huntington's disease and (optionally in combination with GDNF) CC diner ear sensory neurons. The receptor can also be used to block CC unwanted GDNF activity, analyse GDNF related molecules and cells, preferably transfected ex vivo, can be used similarly by CC diner responsive cells and the use of the receptor CDNA in gene therapy is CC also contemplated. Probes based on the CDNA can be used to identify could benefit from GDNF therapy, and abnormalities in receptor CC expression, and to isolate molecules that form a complex with the CC would benefit of solate molecules that form the CDNA, and animal condities, oligonucleotides derived from the CDNA. Anti-receptor CC expression, and to isolate molecules that form the CDNA, and animal condities, oligonucleotides derived from the CDNA. Anti-receptor CC antibodies, oligonucleotides derived from the CDNA, and animal condities, oligonucleotides derived from the CDNA, and animal condities of increasing dopamine uptake in dopaminergic cells.

CC can be used in immunoassays for the receptor. The receptor binds complex that mediates/enhances signal transduction by GDNF, i.e. CC increasing dopamine uptake in dopaminergic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treat dopaminergic nerve cell disorders, e.g. Parkinson's Alzheimer's disease Claim 1; Pages 96-98; 196pp; English.
 434
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                hittksmaappscslsslpvlmltala 457
                                                                                                                      KLNSGSSRARLSAALTALPLLMLT-LA
                                                                               LASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKC
                                                                                                                                                                                                                                                                                                                                    lmsaevsg-gdrldcvkasdqclkeqscstkyrtlrqcvagketnfsltsgleakdecrs
| ::|: | ::|||:|: | | :|||||||||:||: | :: | | | | ||::
                                                             -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKV; a ::
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No. 1.20e-147;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 14:28:13 1999; MasPar time 23.75 Seconds 725.580 Million cell updates/sec

Tabular output not generated.

Run on:

Title:

Description:
Perfect Score:
Sequence: >US-08-866-354-40 (1-460) from US08866354.pep 3343 1 MLVFPSHYPDETLRSLASPS.....RARLSAALTALPLLMLTLAL 460

Scoring table: PAM 150 Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.747; Variance 80.467; scale 0.581

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match I 23.2 3.1 102 3.1 103 3.1 106 2.9 96 2.9 95 2.8 92 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7 99 2.7	
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JE0082 WEBE9 WABE9 A39261 A47096 S72723 S72723 S72723 S72723 S72723 S52366 G64322 S13588 DEMZMC S6466 DEMZMC S6466 TVRTTB A5567 TVRTTB A55567 C70927 S11587 S11587 A40963 A449663 A449663 A449663	
Description GPI-linked receptor - gene 9 protein - huma masking protein precu response regulator ho dipeptide transport p probable cinA - Mycob zinc finger protein 1 hypothetical protein hypoxia-inducible gen malate dehydrogenase translation elongatio translation elongatio translation elongatio fibrillin 1 precursor fibrillin 1 precursor fibrillin 1 protein malate dehydrogenase probable plysophosphat cysteine proteinase (cysteine proteinase (cysteine proteinase (galactose-1-phosphate	
4.61e-149 1.31e-01 9.37e-02 9.15e-01 4.66e-01 4.83e-01 9.15e+00 3.18e+00 3.	

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nerve growth factor r probable transmembran	Ca2+/calmodulin-depen	integral membrane pro	mucin 2 precursor, in		fibrillin-2 precursor	fibrillin-2 precursor	ascites sialoglycopro	probable hormone rece	probable transcriptio		C05B5.5 protein (clon	probable phosphoester	epidermal growth fact		malate dehydrogenase	malate dehydrogenase	tRNA isopentenyltrans	decay-accelerating fa	UTPhexose-1-phospha
1.06e+01 1.06e+01	1.06e+01	1.06e+01	5.83e+00	5.83e+00	7.85e+00	5.83e+00	5.83e+00	5.83e+00	7.85e+00	7.85e+00	4.31e+00	5.83e+00	7.85e+00	5.83e+00	5.83e+00	5.83e+00	4.31e+00	4.31e+00	5.83e+00

ALIGNMENTS

YTYRMLFCSC-QDQA-CAERRRQTILPSCSYEDKEKPNCLDLRSLCRTDHLCRSRLADFH 268	ILFCSC-QDQA-CAE	Qy 211 YTYRM
CAPEDAGCGERRRNTIAPSCALPS-VTPNCLDLRSFCRADPLCRSRLMDFQ 266	LLCPCAPEDAGCGE	Db 208 HAQGL
STKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRKCHKALROFFDRVPSE 210	HCLDAAKACNLNDN	Qy 151 STKSN
FAMICTLHDKCDRLRKAYGEACS-GIRCQRHLCLAQLRSFFEKAAES	CLKFAMLCTLHD	Db 153 KPDSD
KRGMKKELQCLQIYWSIHLGLTEGE-EFYEASPYEPVTSRLSDIFRLASIFSGTGTDEAN	KELQCLQIYWSIHI	Qy 92 KRGMK
CLDIYWTVHPARSLGDYEL-DVSPYEDTVTSKPWKM-NL-S-K-I,N-:	HOATCLDIYWTVHE	Db 101 HRRMK
CVRANELCAAESNCSSRYRTLRQCLAGRDRNTML - ANK ECQAALEVLQESPLY	VELCAAESNCSSRYF	Qy 36 CVRAN
ANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC 10	RKCEANPACKAAYO	Db 41 CTOAR
23.2%; Score 777; DB 2; Length 397; rity 38.5%; Pred. No. 4.61e-149; onservative 74; Mismatches 99; Indels 25; Gaps '"	Query Match 23.2%; Best Local Similarity 38.5%; Matches 124; Conservative	Query Match Best Local Si Matches 124
predicted #length 397 #molecular-weight 44307 #checksum 2962	#length 397	SUMMARY
#region hydrophobic\ #binding_site carbohydrate (Asn) (covalent) #statu	#regior	380-397 92,145,306
#domain signal sequence #status predicted #label s	#domair	FEATURE 1-25
ycoprotein	glycoprotein	w
##CTOSS-TeleTences DBJ:AB008833; NID:9262/159; PID:92627160 This protein plays a distinct role in cell survival and	protein plays	COMMENT This
	##residues 1-397 #	##residue
0082	JE0082	#accession
novel cDNA related to GDNFRalpha and NTNRalpha.	Molecular cl	#title
Biochem. Biophys. Res. Commun. (1998) 244:849-853	Blochem. Bio	# journal
COOK	NOTO S .	#AUT hors
00082 00082	JE0082	ACCESSIONS
#formal_name Mus musculus *common_name house mouse 21.May-1998 *text_change		ORGANISM DATE
	GPI-linked GFRalpha-3	TITLE ALTERNATE NAMES
0082 #type complete	JE0082 #	RESULT 1

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RESULT
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#journal
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#accession A38261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Davison, A.J.; Scott, J.E.
#journal J. Gen. Virol. (1985) 67:1759-1816
#title The complete DNA sequence of varicella-zoster virus
#cross-references MUID:86306657
                                                                                                             ##cross-references GB:M55431; NID:g207285; PID:g207286
|FICATION #superfamily LDL receptor ligand-binding repeat homology
| #length 1712 #molecular-weight 186598 #checksum 9047
                                                                                       155 NHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKCH 197
                                                                                                                                                                   y match
Local Similarity 34.9%;
hes 15.
                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                         ##Status
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##residues 1-302 ##label DAV
##cross-references EMBL:X04370; N
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hes 16; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  masking protein precursor - rat
#formal_name Rattus norvegicus #
14-Jun-1991 #sequence_revision 1
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                   Tsuji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8835-8839
Molecular cloning of the large subunit of transforming growth
factor type beta masking protein and expression of the mRNA
in various rat tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily varicella-zoster virus gene 9 protein
#length 302 #molecular-weight 32846 #checksum 3700
       response
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gene 9 protein - human herpesvirus 3
#formal name human herpesvirus 3, varicella-zoster virus
30.Sep-1988 #sequence_revision 30-Sep-1988 #text_change
                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                    1-1712 ##label TSU
                                                                                                                                                                                                                                                                                                                  preliminary
     #type complete
regulator homolog
                                                                                                                                                                            Score 103; DB 2;
Pred. No. 9.37e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 1; Length 302; Pred. No. 1.31e-01; 15; Mismatches 23; Indels
   homolog,
                                                                                                                                                             Mismatches
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 aerial mycelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #common_name Norway rat
14-Jun-1991 #text_change
                                                                                                                                                                                            Length 1712;
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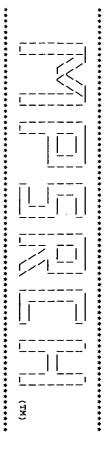
Parkhill,

J.;

Garnier,

T.;

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                                                                                                                                                                         h 2.9%;
Similarity 37.2%;
16; Conservative
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dipeptide transport protein precursor homolog
Mycobacterium leprae
IES B117_C1_166 protein
#formal_name Mycobacterium leprae
19-Mar-1997 #sequence_revision 25-Apr-1997 #t.
09-Sep-1997
572723
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Similarity 34.5%;
10; Conservative
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GTG
#length
B70518 #type complete
probable cinA - Mycobacterium tuberculosis (strain H37RV)
#formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                            Smith, D.R.; Robison, K. submitted to the EMBL Data Library, November Mycobacterium leprae cosmid B1177. $72723
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J. Bacteriol. (1993) 175:2006-2016
A gene cluster involved in aerial mycellum formation in
Streptomyces griseus encodes proteins similar to the
response regulators of two-component regulatory systems
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Pred. No. 6.66e-01
11; Mismatches 1
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Pred. No. 9.15e-01;
11; Mismatches 8
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Mar 8 14:30:24 1999; MasPar time 16.69 Seconds 739.585 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-866-354-40 (1-460) from US08866354.pep 3343 1 MLVFPSHYPDETLRSLASPS.....RARLSAALTALPLLMLTLAL 460

Scoring table: PAM 150 Gap 11

Searched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot36 1:swissprot

Statistics: Mean 48.125; Variance 69.852; scale 0.689

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222223	٠,-	Result
26150 26150 11560 11514 11514 1032 1032 1032 1032 1032 1032 1032 1032	3196	Score
4444444 444668 444668 4444 4444 4444 44	95.6	Query
464 468 468 468 469 469 410 354 1712 1712 1712 174 432 432 443 445 452 452 463 463 463 463 463 463 463 463 463 463	463	Length
	ъ.	B
NRTR CHICK GDNR_RAT GDNR_MOUSE GDNR_CHICK GDNR_HUMAN UL49_V2VD TGEB_RAT NOV_MOUSE Y182_MSTJA MDHC_SGRBI MDHC_MAIZE NOSS_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN EFTU_HUMAN	NRTR_MOUSE	ΠŪ
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THYROID PEROXIDASE PRE	NEL PROTEIN PRECURSOR	HIGH AFFINITY NERVE GR	INOSINE-5'-MONOPHOSPHA	ESTRADIOL 17 BETA-DEHY	L-ALLO-THREONINE ALDOL	MUCIN 2 PRECURSOR (INT	FIBRILLIN 2 PRECURSOR.	FIBRILLIN 1 PRECURSOR.	PUTATIVE VITELLOGENIN	CELL SURFACE GLYCOPROT	PHOSPHORUS ACQUISITION	NEL PROTEIN PRECURSOR	GLYCOPROTEIN B PRECURS	PHOSPHOLIPASE A-2-ACTI	HYPOTHETICAL 66.5 KD P	TYPE I RESTRICTION ENZ	MALATE DEHYDROGENASE (TRNA ISOPENTENYLTRANSF	COMPLEMENT DECAY-ACCEL	GALACTOSE-1-PHOSPHATE	CATHEPSIN B-LIKE CYSTE
			A	ند. د. د.	4.520.00	1.68	2.350-0	1.68("	1.68e+?"	1.680:00	2.36e+00	1.19e÷∪∪	2.36e+0€	2.36e-(10	1.19e+00	1.68e+00	1.68e+00	1.19e+00	1.19e+00	1.68e+00	1.19e+00

ALIGNMENTS

8======================================	RESULT NO DIT O DIT O O O O O O O O O O O O O O O O O O O
SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 97325791. BALOH R.I., TANSEN HEUCKEROTH R.O., F JOHNSON E.M. JR., NEURON 18:793-802(-1- FUNCTION: RECEPTOR: AUTOPHOSPHORYI TO MEDIATE GD RECEPTOR: -1- TISSUE SPECIFIA ROOT GANGLIA, AND IN THE ADD -1- ALTERNATIVE PR SPLICING: -1- SIMILARITY: BE EMBL; AF002701; GZ MGD; MGI:1195462; MGD; MGI:1195462; RECEPTOR; GLYCOPR ALTERNATIVE SPLICI SIGNAL 1 CHAIN 22 PROPEP 444 CARBOHYD 357 CARBOHYD 357 CARBOHYD 443 VARSPLIC 14 SEQUENCE 463 AAA	NRTR_MOUSE STAN OO8842; O1-NOV-1997 (REL. 3 O1-NOV-1997 (REL. 3 O1-NOV-1998 (REL. 3 NEURTURIN RECEPTOR BETA RELATED NEUROT (GDNFR-BETA). GFRA2 OR GDNFRB OR MUS MUSCULUS (MOUSE EUKARYOTA; METAZOA; EUTHERIA; RODENTIA.
OCHECON NEC	DAR 5, ALP ROP CH
1.G., GOLDEN J.P., CRE. K. C.L., ZIMONJIC D.B. LEBRANDT J.; 197). ON FOR NEURTURIN. MED TON FOR NEURTURIN OF SIGNALING THROUGH THE SIGNALING THROUGH THE SUCTS: A SHORT FORM IS DUCTS: A SHORT FORM IS DOTENTIAL. SO POTENTIAL. 143 GPI-ANCHOR () 143 GPI-ANCHOR () 143 GPI-ANCHOR () 144 MISSING (IN : 1559 MW; OA2165CO C:	ARD; PRT; 463 AA. , CREATED) , LAST SEQUENCE UPDATE) , LAST ANNOTATION UPDATE) LPHA PRECURSOR (NINR-ALPH OPHIC FACTOR RECEPTOR 2) RNR2. CHORDATA; VERTEBRATA; TET
CREEDON D.B., POP D.B., POP D.B., POP H THE RET O THE MEMB HE SUPERIO D TESTIS. RM IS PROD FAMILY. FAMILY. MEMBRANE: AL.	PRT; 463 AA. TED) SEQUENCE UPDATE) RANNOTATION UPDATE) RECURSOR (NTNR-ALPHA) FACTOR RECEPTOR 2) (FACTOR RECEPTOR TETRA
N.C., NRTN-INDUCED ECCEPTOR. ALSO INE KINASE BY A GPI-ANCHO VICAL AND DORS EVEL IN THE SE EVEL IN THE SE EVEL FACTOR MATURATIVE DTROPHIC FACTOR URING MATURATI	A. (TE) (ICPHA) (NRTNR-ALPHA) (TGF- (GDNF RECEPTOR BETA) TETRAPODA; MAMMALIA:
O ABLE HOR (BY SPLEEN SPLEEN TION	·

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Query Match Best Local Similarity

95.68; Larity 96.98; Conservative

. 68;

Score Pred. 9; N

Mismatches 3196; DB 1; No. 0.00e+00;

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Gaps

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71

Length Indels

Matches

438;

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THE WELL BOUND COUNTY OF THE SECOND COUNTY OF THE S
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                                                              ANDELINE; 9735791.

A BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

A HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,

A JOHNSON E.M., JR., MILBRANDT J.;

A JOHNSON E.M., JR., MILBRANDT J.;

C -!- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED

AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABI

C TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE

TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE

C TO MEDIATE COLATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IN SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IN SULLARITY).

C -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IN SULLARITY: BELONGS TO THE GDNFR FAMILY.

SPLICING IN BOTH BRAIN AND PLACENTA.

C -!- SIMILARITY: BELONGS TO THE GDNFR FAMILY.

BR MIM; 601956; -.

R RICHERORY GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;

NATHERNATIVE COLOR OF TAXABLE BY A SIGNAL;

NATHERNATIVE GRANDER GRANDER SIGNAL;
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01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (TGF-
NEURTURIN RECEPTOR ALPHA PRECURSOR RECEPTOR 2) (GDNF RECEPTOR BETA)
                            ALTERNATIVE SIGNAL
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EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GDNFR-BETA).
GFRA2 OR GDNFRB OR TRNR2.
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                SEQUENCE FROM N.A.

TISSUE--BRAIN;

TISSUE--BRAIN;

BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSO ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M. NATURE 387:721-724(1997).

-I-FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NET AUTOPHOSEPHORYLATION AND ACTIVATION OF THE RET RECE TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINI RECEPTOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY INSTALLARITY: BELONGS TO THE GDNFR FAMILY.

EMBL: U90542: G2213805; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                     NRTE_CHICK STANDARD; PRT; 465 AA.
013157;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA)
RECEPTOR BETA) (GDNFR-BETA).
GFRA2 OR GDNFRB.
                                                                                                                                                                                                                                                                              GALLUS GALLUS (CHICHEUKARYOTA; METAZOA; GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
LIPID
VARSPLIC
SEQUENCE
    RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPER
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||:|||| |||:||| ||| |::||| ||
|GSKKVIKLNSGSSRARLSAALTALPLLMLTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNVSPKGPSFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%;
Similarity 94.0%;
    GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AA;
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357
413
444
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                                                                                                                                                                                                                                                                                                                   (CHICKEN)
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413
444
146
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  GPI-ANCHOR;
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HYDROPHOBIC, REMOVED DUR:
(POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR (POTENTIAL).
MISSING (IN SHORT FORM).
M; 3C74BBFB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 3120; DB 1;
Pred. No. 0.00e+00;
17; Mismatches 10
                                                                                                                                                                          BUCHMAN V.L., DAVIES A.M.;
                                                                                                                                                                                                                                                                                              VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 10;
MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464
                                                                                                                                                                                                                                                                                              TETRAPODA;
                                                                                            S THE NRTN-INDUCED
RET RECEPTOR. ALSO
TYROSINE KINASE
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            (NRTNR-ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                           ВΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464;
                                                           GPI-ANCHOR
                                                                                                                                                                                                <u>.</u>
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GDNR_RAT

GDRAP97;

GD1-NOV-1997 (REL. 35, CREATED)

T 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

T 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

E GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RE

E NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).

E NEUROTROPHIC FACTOR RECEPTOR 1)

E NEUROTROPHIC FACTOR RECEPTOR 1;

E GFRA1 OR GDNFRA OR TRNR1 OR RETL1.

S RATTUS NORVEGICUS (RAT).

S RATTUS NORVEGICUS (RAT).

S RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                JING S., WEN D., YU Y
ANTONIO L., HU Z., CUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
LIPID
SEQUENCE
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CHAIN
PROPEP
SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-KIDNEY;
MEDLINE; 9732356.
SANICOLA M., HESSION C.A., WORLEY D.S.,
WALUS L., ROBINSON S., JAWORSKI G., WEI
                                                                                                        TISSUE-RETINA;
                                                                                                                                  EUTHERIA; RODENTIA.
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 370
                                                                                                                                                                                                                                                             425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85:1113-1124(1996).
                                                                                                                                                                                                                                                           ISPGSKKVIKLNSGSSRARLSAALTALPLLMLTLAL 460
                                                                                                                                                                                                                                                                             TMPDQKTFVDQKAAGSRHRAARILPAVPIVLLKLLL 465
                                                                                                                                                                                                                                                                                               ATQAPRVEKTPSLPDDLSDSTSL-GTSVITTCTSIQEQGLKANNSKELSMCFTE--LTTN
                                                                                                                                                                                                                                                                                                         SNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLP
                                                                                                                                                                                                                                                                                                                                            LDLRSLCRTDHLCRSRLADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVD
                                                                                                                                                                                                                                                                                                                                                                                LDLRNVCRADHLCRSRLADFHANCQASFQSLTSCPGDNYQACLGSYTGLIGFDMTPNYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.2%;
Similarity 75.2%;
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387
412
445
465
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22
446
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                                                                           CUPPLES
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387
412
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445
465
                                                                           HOLST I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2615; DB 1; Length 465
Pred. No. 0.00e+00;
67; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI-ANCHOR (POTENTIAL).
; 5CA073E4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

NEURTURIN RECEPTOR ALPHA.

NEUROPHOBIC, REMOVED DURING MATURATION

(POTENTIAL).
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                                                                          P.L., L
                                                                           S J.-C.,
   CARMILLO P., E. H., TIZARD R.,
                                                                                                                                                                   (TGF-BETA
                                                                          FANG M., TAMIR
HU S., ALTROCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 465;
     ., WHITTY
                                                                                                                                          MAMMALIA;
                                                                                                                                                                              RELATED
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AB BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
AB BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
AB ASAI N., TAKAHASHI M., WOORE M.W., BUJ-BELLO A., DAVIES A.M.,
AND R. BEZEPTOR FOR GONE MEDIATES THE GENEFINDUCED R., HATURE 382:80-83(1996).
C. INATURE 382:80-83(1996).
C. INATURE 382:80-83(1996).
C. INATURE 382:80-83 FOR GONE MEDIATES THE GENEFINDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
C. INATURE 2 MOLECULES OF GONER-ALPHA ARE THOUGHT TO FORM A CONCILING CONTROL OF THE RET RECEPTOR.
C. INSUBURTE: 2 MOLECULES OF GONER-ALPHA ARE THOUGHT TO FORM A CONCILING CONTROL OF RESERVENCE OF THE DISCULEDE-LINKED GONE DIMER AND MITH 2 MOLECULES OF RESERVENCE.
C. INSUBURTE DISCULTION: ATTACHED TO THE MEMBARNE BY A GPI ANCHOR.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUBLE CONTROL OF THE GONER FAMILY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
C. INSUB SPECIFICITY: EXPRESSED IN LIVER.
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JLT 5
GDNR_MOUSE
P97785;
01-NOV-1997
01-NOV-1997
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CARBOHYD
LIPID
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CARBOHYD
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PROC. NATL. ACAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LMSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HITTKSMAAPPSCSLSSLPVLMLTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                     PWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMMQPAPPVQTTTATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
                                                                                                                                                                                                                                                                                                                                                    FRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASS
                                                                                                                                                                                                                                                                                               -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKV!
                                                                                                                                                                                                                                                                                                                                                                                                         PWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRV-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 46.7%;
Similarity 48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362
59
347
406
430
468 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
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59
347
406
430
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SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51649 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1560; DB 1;
Pred. No. 0.00e+00;
98; Mismatches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

GDNF RECEPFOR ALPHA.

HYDROPHOBIC, REMOVED

(POTENTIAL).

POLY-THR.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
GPI-ANCHOR (POTENTIAL).
6A7A2B2A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94:6238-6243(1997).
                                                                                                                                                                                                                                             457
                                                                                                                                                                                           459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 117; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMOVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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(REL. 35, CREATED) (REL. 35, LAST SEQ

SEQUENCE

UPDATE)

STANDARD;

468 ጅ

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Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
-!- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-I
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RE
SIMILARITY).
-!- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT
WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB000800; G
MGD; MGI:1100842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (
NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR;
  434
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                                                                                                                                                                                                                                            137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                    AMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR
                                                                                                                                                                                                                                                                                                                                                LMSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNESLTSGLEAKDECRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
KLNSGSSRARLSAALTALPLLMLT-LA
                                           -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVI
                                                          PWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPVQTTTAMTTTA
                                                                                                                                         DHLCRSRLADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVS
                                                                                                                                                      HKALRQFFDKVPAKHSYGMLFCSCRDVACTERRRQTIVPVCSYEERERPNCLNLQDSCKT
                                                                                                                                                                                                                                                  AVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTTSMS-NEVCNRRKC
                                                                                                                                                                                                                                                                                                                                  LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
                      HITTKSMAAPPSCGLSSLPVMVFTALA 457
                                                                                         PWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQA-PRVE
                                                                                                                                                                                        HKALROFFDRVPSEYTYRMLFCSCODOACAERRROTILPSCSYEDKEKPNCLDLRSLCRT
                                                                                                                                                                                                                                       LASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKC
                                                                                                                                                                                                                                                                                    ALEVIQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB000800; G1816442;
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN; GPI-ANCHOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                  347
406
430
468
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431
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51782
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59
347
406
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1541; DB 1; I
Pred. No. 0.00e+00;
103; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROPHOBIC, (POTENTIAL).
THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GDNFR-ALPHA) (TGF-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                  6C64C182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDNFR
 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATA BANKS.
THE GDNF-INDUCED
THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY A GPI-ANCHOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO FORM A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATURATION
                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF RET
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                    430
                                                                                                                  370
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Best Local S
Matches 22
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CARBOHYD
CARBOHYD
LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDNR_CHICK STANDARD; PRT; 469 AA. 0.13156; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (GRAIOR GDNFRA. GERALOR GDNFRA. GERALOR GDNFRA. GREATOR RECEPTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE T
WITH THE DISULFIDE-LINKED GDNF DIMER AND
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
BUJ-BELLO A., ADU J., PINON L.G.P., F
ROSENTHAL A., CHINCHETRU M., BUCHMAN
NATURE 387:721-724(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALLUS GALLUS (CHICKEN)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLIFORMES
                                        379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
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                                                              328
                                                                                                                                                                                                                 145
                                                                                  321
                                                                                                        268
                                                                                                                             263
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                                                                                                                                                                                                                                                                                       29 RLDCVKASDQCLKEQSCSTKYRTLRQCVAGKESNFSRATGLEAKDECKSAMEALKQKSLY ::|||:||:||::||::||:::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTOPHOSPHORYLATION AND SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE AUTOPHOSPHORYLATION AND ACTIVATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                    TTNNEIPTHNDSPACANLQAQKKRKSNESVDTELCLNENAIGKDNTPGVSTS-HISSENS
                                                                                                   STS--LGT-SVITTCTSIQEQGL-KANNSKELSMCFTE--LTTNISPGSKKVIKLNSGSS
                                                           EEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPA-TQAPRVEKTPSLPL: 8
                                                                                                                                              PSEYTYRMLFCSCODOACAERRRQTILPSCSYEDKEKPNCLDLRSLCRTDHLCRSRLADF
                                                                                                                                                         PPKHSYGMLFCSCRDVACTERRRQTIVPVCSYEDREKPNCLNLQESCKKNYICRSRLADF
                                                                                                                                                                                        PAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFDRV
                                                                                                                                                                                                       PVLS-KGNNCLDAAKACNLNDTCKRFRSAYITPCTSSTS-NEICNKRKCHKALRLFFDKV
                                                                                                                                                                                                                                                                            QVDCVRANELCAAESNCSSRYRTLRQCLAGRD----RNTMLANK-ECQAALEVLQESPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U90541;
                                                                                                                                                                                                                                                                                                                         l Similarity
221; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                   469
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                                                                                                                                                                                                                                                                                                                                  45.48;
                                                                                                                                                                                                                                                                                                                                                                            368
62
163
346
405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE
                                                                                                                                                                                                                                                                                                                        Score 1519; DB 1;
Pred. No. 0.00e+00;
99; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

GDNF RECEPTOR ALPHA.

HYDROPHOBIC, REMOVED

(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
GPI-ANCHOR
C8D241C9
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDNFR FAMILY.
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N V.L.,
                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A., THOMPSON DAVIES A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THOUGHT D WITH 2
                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TGF-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                            Length 469;
                                                                                                                                                                                                                                                                                                                      Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY A GPI-ANCHOR (RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO FORM A COMPLEX MOLECULES OF RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVES: NEOGNATION:
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                   262
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Best Local
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CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) ('NEUROTROPHIC FACTOR RECEPTOR 1).
GFRA1 OR GDNFRA OR TRNR1.
HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOX G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SUBSTANTIA NIGRA; MEDLINE; 96270513.
JING S., WEN D., YU Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNR_HUMAN P56159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTONIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - | SIMILARITY: BELONGS
                                                                                                                                            137
                                                                      252
                                                                                              197
                                                                                                                     193
                                                                                                                                                                   134
  317
                                               257
                                                                                                                                                                                           77
                                                                                                                                                                                                                75
                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: ATTACHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.M.;
85:1113-1124(1996).
FUNCTION: RECEPTOR FOR GDNF. MEDIATES
FUNCTION AND ACTIVATION OF
                                                          NYICRSRLADEFINCQPESRSVSSCLKENYADCLLAYSGLIGTVMTDNYIDSS-S-LSVA 309
                                                                                                         HKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEEREKPNCL-LQDSCKT
                                                                                                                                                                                                                                       LQGSELHGWRPQVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-TM---LANK-ECQA
                                                                                                                                                                                                                                                    LLSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRS
                                                                                                                                          LASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKC
                                                                                                                                                                 VVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS-NDVCNRRKC
                                                                                                                                                                                                      AMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFR 133
             PWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGSDVTVWQPAPPVQTTTATTTTA
PWCNCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRV-E
                                             DHLCRSRLADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVS
                                                                                                                                                                                         ALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFR
                                                                                            HKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYEDKEKPNCLDLRSLCRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., WEN D., YU Y., HOLST P.L., LUO Y., FANG MO L., HU Z., CUPPLES R., LOUIS J.-C., HU S.,
                                                                                                                                                                                                                                                                                    th 45.3%;
Similarity 50.6%;
206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                      464
                                                                                                                                                                                                                                                                                                                                                                                                                     25
429
                                                                                                                                                                                                                                                                                                                                      <u>Α</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                            368
59
346
405
428
51291
                                                                                                                                                                                                                                                                                                                                                                                                                     428
464
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPI-ANCHOR; MEMBRANE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                    Score 1515; DB 1; 1
Pred. No. 0.00e+00;
92; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  POLY-THR.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                    GPI-ANCHOR
2C8C3574
                                                                                                                                                                                                                                                                                                                                                                                                                     GDNF RECEPTOR ALPHA.
HYDROPHOBIC, REMOVED DURING
                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE GDNF-INDUCED
THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TGF-BETA RELATED
                                                                                                                                                                                                                                                                                                          Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., TAMIR
                                                                                                                                                                                                                                                                                     Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTROCK B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                      MATURATION
                                                                                                                                                                                                                                                                                    Gaps
                       369
                                                                                                                                                                                         136
                                                                                                                                                                                                                                       76
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                                                                                                                                          196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UL49_VZVD
P09272;
01-MAR-1989
01-MAR-1989
01-DEC-1992
                                                                                    SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGFB_RAT STANDARD; PRT; 1712 AA..

Q00918;

Q1-JUL-1993 (REL. 26, CREATED)

Q1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)

Q1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

LATENT TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1 PRECIDENT:

(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA-1-4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVISON A.J., SCOTT J.E.;
J. GEN. VIROL. 67:1759-1816(1986).
-I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,
EHY-1 11, AND VZV 9.
EMBL; X04370; G59998; -.
PIR; IZ7212; WZB59.
                                                                                                                                                                                                           PROSITE; PS00010; ASX_HYDROXYL;
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 10.
PROSITE; PS01187; EGF_CA; 15.
                                                                                                                                                                                                                                                                                                                                                           A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE -:- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS. EMBL, M55431; G207286; -. PIR; A38261; A38261.
HSSP; P19398; 1ATA.
                                                                                                                                                                                      GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 86306657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARICELLA-ZOSTER VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., MEDLINE; 91062373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /IRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEGUMENT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TRANSFORMING GROWTH FACTOR BETA-1 MASKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LCRSNAVRRKTTPSYSGQYRTARRSVVVGPPDDSDDSLG-YITTVGADSPSPVYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KTPSLPDDLSDSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCRTDHLCRSRLADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDM-TPNYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLCISN
                                                                                                                                                                                         FACTOR BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 3.1%;
Similarity 28.6%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DS-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REL. 10, CREATED)
(REL. 10, LAST SEQUENCE UP
(REL. 24, LAST ANNOTATION
OTEIN (GENE 9 PROTEIN).
                                                                                           21
737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R VIRUS (STRAIN DUMAS)
ENVELOPED VIRUSES; HEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32846 MW;
                                                                                                                                                                                         REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102; DB 1;
Pred. No. 2.17e-02;
15; Mismatches 2;
POTENTIAL.
POTENTIAL.
POTENTIAL.
LATENT TRANSFORMING GROWTH FACTOR BETA
BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                      EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901F3DC4
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HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                      DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 302
                                                                                                                                                                                      HYDROXYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAKGE
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4.

Gaps

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REPEAT
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Ret ligand; RetLi; RetCaptor; signal transduction; mouse; well growth; renal cell; nerve cell; renal failure; nephritis; well growth; tenal cell; nerve cell; renal failure; nephritis; weldney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; neurodegeneration; motor neurone disease; multiple sclerosis; neurodegeneration; meningitis; myelopathy; Creutzfeldt-Jakob disease; we cranial nerve injury; spinal cord injury; Down's syndrome; we crebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                                                                                                                                                                       W09744356-A2.
27-NOV-1997; U07726.
10-APR-1997; US-017427.
10-APR-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021899.
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel M; WPI; 98-018431/02.
P-PSDB; W37465.
New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or nerve cells

Disclosure; Page 71-73; ll3pp; English.

This sequence comprises EST AA050008, identified as a partial cDNA for mouse Ret ligand (RetL) RetL3 (see W37455), by sceening of an EST database with rat RetL1 (see W37457). A full-length mouse retL3 cDNA clone (see V00249) was obtained by combining
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Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T;
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08-MAY-1996; US-0174,
07-JUN-1996; US-0193,
16-JUL-1996; US-0218;
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, s
WPI; 98-018431/02.
P-PSDB; W37461.
                                                                                                                                                                                                                                                                                                       W09744356-A2.
27-NOV-1997.
07-MAY-1997; [
nerve cells

claim 1; Page 75-77; 113pp; English.

This sequence comprises cDNA coding for mouse Ret ligand (RetL)

RetL3 (see W37461), a key component of the Ret signalling pathway.

It was deduced from a partLal clone (see V00256) obtained from

from an EST database search with rat RetL1 (see W37457) and from

a clone obtained by 5' RACE. Rat and human retL1, and human retL2

and retL3 DNA sequences are also claimed (see V00245-48 and

v00250-51). Vectors containing retL3 DNA and prokaryotic or

eukaryotic host cells transformed or transfected with these vectors

are claimed, as well as a method for production of RetL3, its
                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Ret ligand retl3 cDNA.

Ret ligand; RetL3; receptor; signal transduction; mouse cell growth; renal cell; nerve cell; renal failure; nephrilis kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                                                                                                                                                New nucleic acid encoding ret receptor ligands and related prot. vectors, transformed cells and antibodies, used for promoting growth and improving survival of injured cells, especially renal
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27-NOV-1997; U07726.
07-MAY-1997; US-017427.
08-MAY-1996; US-017427.
07-UN-1996; US-01300.
16-UU1-1996; US-01859.
(BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel MWPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Ret ligand retL3 cDNA.

Ret ligand; RetL; RetL3; receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; miltiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
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                                           New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
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Claim 1; Pag
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So Sequence 1699 BP; 328 A; 562 C; 468 G; 341 T;
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Best Local Similarity
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ilarity 82.3%;
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                                                                                                         Cate RL, Hession C, Sanicola-Nadel WPI: 98-018431/02.
P-PSDB: W37462.
New nuclei-
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27-NCV-1997; U0:

07-MAY-1997; US:

10-APR-1997; US:

08-MAY-1996; US:

07-JUN-1996; US:

16-JUL-1996; US:

16-JUL-1996; US:

16-JUL-1996; US:
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21-MAY-1998 (first entry)

Ret 11gand; RetL3 partial cDNA clone GJ128.

Ret 11gand; RetL3; Receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy; ss.
                                                New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
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So Sequence 1271 Bp; 264 A; 414 C; 316 G; 277 T;
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Q51746 standard; cDNA; 91 BP.
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; my
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Q51746 standard; q
Q51746; standard; q
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G14MY 1994 (firs
Oligonucleotide pa
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Oligonuclectide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested. cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligo:nucleotide probes specific for Mycobacteria detection and amplification of Mycobacteria nucleic ac
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                                                                                                                                                                                                                                                                                                gcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvhhvvhvvhhvhyhvyvsv
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                                                                                                                                                                                                                                                                                                                                                n 2.5%;
Similarity 3.8%;
2; Conservative
                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                              Score 43; DB 9;
Pred. No. 2.20e-
46; Mismatches
                                                                                                                                                                                                                                                                                                                                         DB 9;
2.20e-11;
--hes 5;
                                                                                                                                                                                                                                                                                                                                                                                              Length
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ss. Synthetic. EP-571911-A.

(first entry)
ide probe MK14-A DNA probe;

mycobacteria; disease diagnosis;

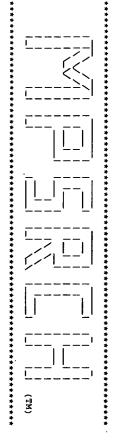
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Best Local s
Matches
                                                                                                                                                               Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                        Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which covers a transcriptase. But the sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-285123-A.
05-MAY-1988; 105163.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40.
                                                                                                                                                                                                                                                                         occurred singularly in any given mutant. See also p80575.
Sequence 204 BP; 21 A; 47 C; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1993;
24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Base substituted E.coli beta-galactosidase alpha-fragment. E.coli beta galactosidase alpha-fragment; base substitutions; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N81164 standard; DNA; 204
N81164;
08-NOV-1990 (first entry)
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New oligo:nucleotide probes specific for Mycobacteria - undetection and amplification of Mycobacteria nucleic acid
154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                837 GTGCAGATCACGCCTGATGGACTTCCAGACCCACTGCCACCCTATGGAC 885
                                                                             95 rrmrbnvyrdynrsdaa-awyccyrrsvkydccynachhddhyvybbbvynvhnhnncnc 153
                                                                                                                                                                                            Local
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                                             Similarity 11.6%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 2.4%;
Similarity 2.0%;
1; Conservative
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                                                                                                                                                                                      2.48;
                                                                                                                                                                                                                                                                      21 A;
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                                                                                                                                                    Score 40; DB 1; Ler
Pred. No. 1.40e-09;
52; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41;
Pred. No.
44; Misma
                                                                                                                                                                                                                                                                      47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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3.54e-10;
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                                                                                                                                                                                                             Length 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elongation,
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RESULT ACCORDING TO THE RESULT
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC 070468 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be crepresented as follows: X(NNB)11(TGC)(NNB)7(TGC)(NNB)10Y. X CC and y are flanking restriction sites (X is not the same as y) that are not specified further. Other generic sequences are shown in 070466-88. CC chemically experides generated by these generic sequences are shown in CC affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSAPS or compsns. comprising a TSAR binding domain can be used in vivo to compsns. comprising a TSAR binding domain can be used in vivo to compsns. peptide, toxin or enzyme, to the specific target we callous tops, peptide, toxin or enzyme, to the specific target we callous or peptide. They can also replace the function of macromolecules, vis. CC production. The TSARs are easily characterised and have designed considered and replace and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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18-AUG-1994; U00977.
01-FEB-1994; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
P-PSDB; R65154.
   Q70466;
Q70466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLT 8
Q70468 standard;
Q70468;
Q5-APR-1995 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion comprising a binding domain and an effector domain Disclosure: Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR petide library, TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1470 GCTTGGGCTGCTCCCTAGGACCTTGTACTCCA
                                                                                                                                                                                                                                                                                       625
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                                                                                                                                                                                                                                                                                                                                 3 bողծողծողծողծողծողծողծողծողծողծեց cողծողծողծողծողծողծողողությո
                                                                                                                                                   TCCCACGCTCAGGGCCTGCTGCTGTGCCCTGTGCACCCGAAGATGCGGGCT
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                                                                                                                                                                                                                                                                    CGCTGCCAGCGCGCTCTGCCTAGCTCAGCTGCGCTCCTTCTTCGAGAAGGCGGCAGAG
                                standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                           9
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/note= "this se
sequence of 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 38;
Pred. No.
33; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents 'Z';
6, 9 or 12 nucleotides (s
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
2.14e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114
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proteins
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Mar 8 14:37:58 1999; MasPar time 14.37 Seconds 447.095 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-866-354-42 (1-397) from US08866354.pep 2962 1 MGLSRSPRPPPLVILLLVLS.....LRLPVLSFFILTLILLQTLW 397

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.465; Variance 144.588; scale 0.238

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 3 3 4 4 3 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
2781 2346 2346 2346 759 779 708 695 695 695 695 995 991 991 991	Score
12222226779 333333556993 44712344559167299	Query Match
33409 44664 4664 4664 4666 4666 4666 4666	Length
221 221 231 231 231 231 231 231 231 231	BG
W37461 W37463 W37465 W37460 W37460 W37450 W37459 W37457 W37457 W37457 W37458 W3	ID
Mouse Ret ligand RetL Human Ret ligand retL Mouse Ret ligand RetL Human Ret ligand RetL Human Ret ligand RetL Human Ret ligand RetL Human get ligand RetL! Rat gilal cell line Rat gilal cell derive Rat gilal cell derive Rat gilal cell ine-d Human IL-7 receptor c BIV env and rev exon Generic anti-obesity Generic ob protein. Generic ob protein. Generic ob protein.	Description
4.98e-267 1.42e-224 1.26e-182 7.26e-185 9.15e-62 2.83e-60 1.06e-55 2.05e-55 2.05e-55 2.05e-55 2.05e-40 1.4.10e-01 4.10e-01 4.10e-01 4.10e-01	Pred. No.

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rchd528 gene product. Human antihaemophilic	conglutinin.	-beta-like	TGF-beta-	-beta-like	-beta	11ke	yonal lung	မွ	'n	nally truncat	70	Ŗ	C-terminally truncate	ly truncat	۲	fr	Prepro-LAP #2.		Sequence of human fac	Chicken cytotactin.	Lysophosphatidic acid	-beta-li	-beta-like	F-beta-like	Human TGF-beta-like c
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cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and fusion proteins with a toxin, imageable compound or radionuclide. RetL3, optionally when expressed from vectors in vivo, is used to	and/or autophosphorylation of the Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or eukaryotic host	a key component of the Ret signalling pathway that specifically interacts with Ret receptor protein, triggering Ret dimerisation	sequences (see W37457-60 and W37462-63) are also claimed. RetL is	deduced from cons crones (see v00249) isolated from an EST database and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3	This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,	Claim 2; Page 77-78; 113pp; English.	nerve cells	lls and antibodies, used for prom	New nucleic acid encoding ret receptor ligands and related protol:	N-PSDB; V00249.	98-018431/02.		EN INC.			08-MAY-1996; US-017427.	US-017427	07-MAY-1997; U07726.	27-NOV-1997.	W09744356-A2.		mvasthenia gravis: timour: therapy.	crantal nerve injury; spinal cord injury; Down's syndrome;	is; m	neurodegeneration; motor neurone disease; multiple sclerosis;	toxic	l cell; nerve cell; renal failure; nephriti	Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;	towns Ret	21-MAY-1998 (first entry)	W37/61. Standard; FIOTEIN; 39/ AM.	1

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10-APR-1996; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-019300.
                                                                                                                                                                                        Human Ret ligand RetL3: "Ceptor; signal transduction; human; Ret ligand; RetL4; RetL3; receptor; signal failure; nephritis; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myssthenia gravis; tumour; therapy.
                                            Cate RL, Hession C WPI; 98-018431/02.
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21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis bacterial, viral or prion infections (e.g. meningitis, myelopathy associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis). Fusion proteins are used to deliver toxins etc. to Ret-expressing sequence 397 AA;
                                                       (BIOJ ) BIOGEN INC.
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| Similarity 92.9%;
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eacid encoding ret receptor ligands and related proteins transformed cells and antibodies, used for promoting cel
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Mismatches 12;
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CC This amino acid sequence comprises human Ret ligand (RetL) RetL3. CC deduced from cDNA clones (see v00251) isolated from a adult heart CC and spinal cord libraries. Rat and human RetL1, human RetL2 and CC mouse RetL3 sequences (see w37457-62) are also claimed. Human CC RetL3 is 34.3% identical to human RetL1, 34.9% identical to human CC RetL3 is 34.3% identical to human RetL1, 34.9% identical to human CC component of the Ret signalling pathway that specifically CC component of the Ret signalling pathway that specifically CC interacts with Ret receptor protein, triggering Ret dimerisation CC vectors containing retL3 DNA and prokaryotic or eukaryotic host collist transformed or transferted with these vectors are claimed, as CC well as a method for production of RetL3. Its soluble variants and CC fusion proteins with a toxin, imageable compound or radionuclide. CC retL3, optionally when expressed from vectors in vivo, is used to CC promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue, Typical applications are in CC renal failure, nephritis, kidney transplants, toxic or hypoxic conjury, neurodegeneration, motor neurone disease, multiple sclerosis, CC bacterial, viral or prion infections (e.g. meningitis, myelopathy CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or Spinal cord injury, developmental disorders such as Down's syndrome CC spinal palsy, or conditions involving the peripheral nervous CC system (Lyme disease, muscular dystrophy and myasthenla gravis). CC cells, especially tumours.
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W37465;
21-MAY-1998 (first entry)
Nouse Ret ligand retL3 partial sequence.
Ret ligand; RetL; RetL3; receptor; signal transduction; cell growth; renal cell; nerve cell; renal failure; neph kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerication; meningitis; myelopathy; Creutzfeldt-Jakob dis

sclerosis;

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ESULI
ID W37462;

AC W37462;

AC W37462;

DT 21-MAY-1998 (first entry)

DE Human Ret ligand RetL3 partial sequence.

KW Ret ligand; RetL3; receptor; signal transduction; human;

KW Ret ligand; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplant; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myslopathy; Creutzfeldt-Jakob disease;

KW cranial nerve injury; spinal cord injury; Down's syndrome;

KW crebral palsy; Lyme disease; muscular dystrophy;
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KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.

Mus musculus.

PN W09744356-A2.

PN W09744356-A2.

PP 10-APR-1997: U07726.

PF 10-APR-1997: US-017427.

PR 10-APR-1996; US-017427.

PR 10-APR-1996; US-017427.

PR 10-APR-1996; US-019300.

PR 16-JUL-1996; US-013859.

PR 16-JUL-1996; US-021859.

PR 16-JUL-1996; US-021859.

PR (BIOJ) BIOGEN INC.

Cate RL, Hesslon C, Sanicola-Nadel M;

PI Cate RL, Hesslon C, Sanicola-Nadel M;

PI Cate RL, Hesslon C, Sanicola-Nadel M;

PR WPI; 98-018431/02.

PR N-PSDB; V00256.

RN-PSDB; V00256.

PR vectors, transformed cells and antibodies, used for promoting cell proproteins of the proposed cells and antibodies, used for promoting cell proproteins of the proposed cells and antibodies.
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Best Local S
Matches 31
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This polypeptide comprises a partial sequence of mouse Ret ligand RetL3, deduced from EST AA050083 cDNA (see V00256). A full-length mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse and human retL1, retL2 and retL3 cDNA sequences (see V00245-51) and encoded polypeptides (see W37457-63) are claimed and can be used in methods for promoting cell growth and improving survival of cells, especially renal or neural cells.

Sequence 346 AA;
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                                                                                                                                                                                                                                                                                                            TVALGCTCRGSGNLQDECEQLEKSFSQNPCLMEAIAAKMRFHRQLFSQDWADSTFSVMQQ
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larity 93.9%;
Conservative
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Pred.
10; M
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. No. 1.24e-222;
Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 25
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07-MAY-1997; U07726.

10-APR-1997; US-017427.

08-MAY-1996; US-017427.

07-JUN-1996; US-019300.

16-JUL-1996; US-021859.
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New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting coll growth and improving survival of injured cells, especially remained.
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Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve cells
Claim 2; Page
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This amino acid sequence comprises a human Ret ligand
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                                                                                                                                                                                                                                                                                                    147
387
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QLEKSFSQNPCLMEAIAAKMRFHRQLFSQDWADSTFSVMQQQNSSPALRPQLRLPVLSFF
                   t1p1i1111s1w
                                                                                                                                              thchpmdilgtcateqsrclraylgllgtamtpnfvsnvntsvalsctcrgsgnlqeece
                                                                                                                                                                                                                      sklnmlkpdsdlclkfamlctlndkcdrlrkaygeacsgphcqrhvclrqlltffekaae
                                                                                                                                                                                                                                                                                                                                                                             AQQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPVRSLGDYELDVSPYEDTVTSKPWKMNL
                                                                                                                                                                                                                                                                                                   SKLSMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSGIRCORHLCLAQLRSFFEKAAE
ILTLILLOTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 66.7%;
Similarity 81.0%;
252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1977; DB 28;
Pred. No. 7.26e-185;
31; Mismatches 28;
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RESULT ID W

LT 5 W37460

standard;

Protein;

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PS Claim 2; Page 69-70; 113pp; English.

CC Italim 2; Page 69-70; 113pp; English.

CC This amino acid sequence comprises human Ret ligand (RetL) RetL2,

CC deduced from a cDNA clone (see V00248) isolated from a human foetal

CC liver library. Rat and human RetL1 and human and mouse RetL3

CC sequences (see W37457-59 and ward and mouse RetL1 is a

RetL2 is 49-18 identical to human RetL1 protein. RetL is a

RetL2 is 49-18 identical to human RetL1 protein. RetL is a

RetL2 is 49-18 identical to human RetL1 protein. RetL is a

RetL2 is 49-18 identical to human RetL1 protein. RetL is a

RetL2 is 49-18 identical to human RetL1 protein. RetL is a

RetL2 is 49-18 identical to receptor protein, triggering Ret dimerisation

CC key component of the Ret synalling pathway that specifically

CC uniteracts with Ret receptor protein, triggering Ret dimerisation

CC vectors containing retL2 DNA and prokaryotic or eukaryotic host

CC vectors containing retL2 DNA and prokaryotic or eukaryotic host

CC vectors containing retL2 DNA and prokaryotic or eukaryotic host

CC vectors containing retL2 DNA and prokaryotic or eukaryotic host

CC vectors containing retL2 DNA and prokaryotic or eukaryotic host

CC vectors containing retL3 DNA and prokaryotic or eukaryotic host

CC vectors containing retL3 DNA and prokaryotic or readionuclide.

CC vectors porteins with a toxin, imageable compound or radionuclide.

CC vectors porteins are unit its use. Typical applications are in

CC promote growth of new tissue and survival of damaged tissue,

CC prince for its vectors in vivo, is used to

CC prince for its vectors in vivo, is used to

CC prince for its vectors in vivo, is used to

CC prince for its vectors in vivo, is used to

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Best Local S
Matches 12
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Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
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Ret ligand; RetL; RetL2; receptor; signal transduction; human cell growth; renal cell; nerve cell; renal failure; nephritis kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
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16-JUL-1996;
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CVTanelcaaesncssryrtlrqc---lagr-drntmlankecqaalevlqesplydcrc | :| | |::|:|| ||:| ||:| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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larity 37.3%;
Conservative
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US-021859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 464;
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         266
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Matches

3 latlyfalp1-ldlllsaevsggdrl-d-cvkasdqclkeqscstkyrtlrqcvagketn 59 LVILLLVLSLWLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQHLDSCTPSL-SS

Local

Similarity

Conservative

Indels 22;

Gaps

19;

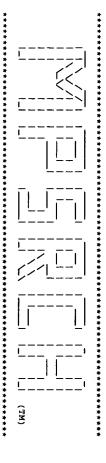
70

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RESULT ACCORDING TO A CONTROL OF THE ACCORDING TO A CONTROL OF THE
                                                                                                                               PT nerve cells

PS Claim 2; Page 64-66; 113pp; English.

CC This amino acid sequence comprises human Ret ligand (RetL) RetL1, CC deduced from cDNA clones (see W00247) isolated from a human CC foetal kidney. Rat RetL1 and mouse and human RetL2 and RetL3 CC sequences (see W37457 and W37460-63) are also claimed. The cc ligand CC interacts with Ret receptor, triggering Ret dimerisation and/or CC interacts with Ret receptor, triggering Ret dimerisation and/or CC containing retL1 DNA and prokaryotic or eukaryotic host cells containing retL1 DNA and prokaryotic or eukaryotic host cells cromptoned or transferted with these vectors are claimed, as well CC contains with a toxin, imageable compound or radionuclide. RetL1, CC optionally when expressed from vectors in vivo, is used to promote CC growth of new tissue and survival of damaged tissue, particularly CC kidney or neural tissue. Typical applications are in renal failure, CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome CC system (Lyme disease, muscular dystrophy and myasthenia gravis). Seguence 460 AA;

Sequence 460 AA;
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                                                                        Query Match
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10-APR-1997; US-017427.
08-MAY 1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
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WPI; 98-018431/02.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Mar 8 14:40:13 1999; MasPar time 21.01 Seconds 707.791 Million cell updates/sec

Run on:

Title:

Description: Perfect Score: Sequence: >US-08-866-354-42 (1-397) from US08866354.pep 2962 1 MGLSRSPRPPPLVILLLVLS.....LRLPVLSFFILTLILLQTLW 397

Scoring table: PAM 150 Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.083; Variance 83.617; scale 0.551

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	SUMMARY #length 397 #molecular-weight 44307 #checksum 2962	Query Match 93.9%; Score 2781; DB 2; Length 397; Best Local Similarity 92.9%; Pred. No. 0.00e+00; Matches 369; Conservative 16; Mismatches 12; Indels 0; Gup:	Db 1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH	OY 1 MGLSRSPRPPPLVILLLVLSLWLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQH 60	Db 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120	QY 121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLSMLKPDSDLCLKFAMLCTLNDKCDKLRKAY(: 19	
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#authors del Sal, G.; Ruaro, M.E.; Philipson, L.; Schneider, C.
#journal Cell (1992) 70:595-607

#title The growth arrest-specific gene, gas1, is involved in suppression.

#cross-references MUID:92370681

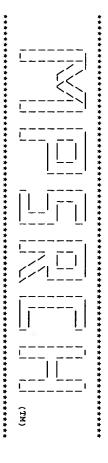
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#title Structure, function, and chromosome mapping of the growth-suppressing human homologue of the murine gas1 gene.
#cross-references MUID:94173926
#accession A53138
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##residues 1-34
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21; Conservative
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#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
__10-sep-1997
                                                               transmembrane protein
#length 384 #molecular-weight 40375
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:es EMBL:X65128; NID:g51045; PID:g51046
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Pred. No. 2.31e-03;
16; Mismatches 22
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REFERENCE A22630
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                                                                                              #authors Nakabeppu, Y.; Sekiguchi, M. (1986) 83:6297-6301
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6297-6301
#title Regulatory mechanisms for induction of synthesis of regulator enzymes in response to alkylating agents: Ada protein as a transcriptional regulator.
#cross-references MUID:86313568
                                                                                                                                                                                                                                                                                                                                                                                                                 #Journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
#title Active site and complete sequence of the suicidal
methyltransferase that counters alkylation mutagenesis.
#cross-references MUID:85190562
#accession A22667
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#accession A22630
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#title
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                                                                                                                                                                                                                                                                                                        ##cross-references GB:M10315; NID:g145190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-133,'R',135-354 ##label NAK ##cross-references GB:M10211; NID:g145188; PI
  ##residues
                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                  ##experimental_source strain B/r
                                                                                                                                                                                                                                                                                                                                                                   ##residues
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NCE A22667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purification and structure of the intact Ada regulatory protein of Escherichia coli K12, O(6)-methylguanine-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptive response regulatory protein - Escherichia coli
methylated-DNA--protein-cysteine S-methyltransferase (EC
2.1.1.63) ada; methylphosphotriester-DNA methyltransferase
#formal_name Escherichia coli
28-Dec-1987 #sequence_revision 05-Dec-1997 #text_change
05-Dec-1997
                                                                           141114
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J. Biol. Chem. (1985) 260:7281-7288
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                                                                                                                                                                                                                                                                                                                                                        1-74, 'D', 76-78, 'PR', 81-317, 'V', 319-329, 'S', 331-384
1-27 ##label RES
                                                translated from GB/EMBL/DDBJ
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##cross-references GB:M13828;

NID:g145196; PID:g145197

1



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 8 14:43:03 1999; MasPar time 31.95 Seconds 685.568 Million cell updates/sec

Title:

Description: Perfect Score:

Sequence: >US-08-866-354-42 (1-397) from US08866354.pep 2962 1 MGLSRSPRPPPLVILLLVLS.....LRLPVLSFFILTLILLQTLW 397

Scoring table: PAM 150 Gap 11

Searched: 180763 segs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb18

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.502; Variance 73.155; scale 0.636

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	BB	Ħ	Description	Pred. No.
1	2781	93.9	397	1	035118	GLIAL CELL LINE DERIVE	0.00e+00
N	2778	93.8	397	11	035325	CELL LINE-	0.00e+00
w	2766	93.4	397	드	055243		0.00e+00
4	2363	79.8	400	4	060609	GDNF FAMILY RECEPTOR A	0.00e+00
G	759	25.6	464	4	015316	GLIAL CELL LINE-DERIVE	1.23e-158
თ	759	25.6	464	4	015328		1.23e-158
7	754	25.5	464	片	035977	GLIAL CELL LINE-DERIVE	2.44e-157
8	744	25.1	460	4	015507	RET LIGAND 1.	9.60e-155
9	742	25.1	463	1	035252	GDNF RECEPTOR BETA.	3.17e-154
10	729	24.6	463	11	035748	GDNFR-ALPHA/TRNR1-DELT	7.44e-151
11	708	23.9	465	4	043912	GPI-LINKED ANCHOR PROT	2.03e-145
12	708	23.9	468	H	035246	GDNF RECEPTOR ALPHA.	2.03e-145
13	690	23.3	431	13	093512	GFR RECEPTOR ALPHA 4 P	9.07e-141
14	103	3.5	339	14	092375	TRANSMEMBRANE PROTEIN.	4.25e-02
15	97	3. 3	159	14	004144	REV PROTEIN 2 (ANTI-RE	3.63e-01
16	97	ນ ພ	253	7	019810	MHC CLASS II DRA.	3.63e-01
17	99	3.3	3291	14	Q66225	ORFA AND ORFB, COMPLET	1.79e-01
18	96	3.2	129	2	082903	PLASMID PO157 DNA, COM	5.14e-01
19	95	3.2	140	N	886690	PUTATIVE TRANSCRIPTION	7.26e-01
20	95	3.2	519	N	Q06919	NITROGEN FIXATION REGU	7.26e-01

45	44	43	42	41	40	39	38	37	36 .	35	34	ω ω	32	3 <u>1</u>	30	29	28	27	26	25	24	23	22	21
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LIPOPHILIC PROTEIN.	CALCIUM .BINDING PROTEI	F11C1.5.	CYTOTACTIN 200KD PRECU	SIMILAR TO EGF-LIKE RE	RESISTANCE PROTEIN REP	SREBP CLEAVAGE ACTIVAT	MAJOR CELL SURFACE GLY	GABA-B RECEPTOR.	KARYOPHERIN BETA2B HOM	GLYCOPROTEIN H.	PUTATIVE G-BINDING PRO	PLACENTAL BONE MORPHOG	HYPOTHETICAL PROTEIN M	BACTERIOFERRITIN COMIG	20	KIAA0199 PROTEIN (FRAG	ENVELOPE GLYCOPROTEIN.	PUTATIVE NEURONAL CELL	HEXAMERIN A (FRAGMENT)	C14B1.9.				
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G1-AUG-1998 (TREMBLREL 07, LAST;

GLAAL CELL LINE-DERIVED NEUROTROP,

GFRA-3.

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VER:

SCIUROGNATHI; MURIDAE; MURINAE; MI
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larity 92.7%;
Conservative
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C., IBANEZ C.F.;
TO EMBL/GENBANK/DDBJ
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2778; DB 11;
Pred. No. 0.00e+00;
17; Mismatches 12
                  PRT;
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E; MUS.
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Matches 36
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PROC. NATL. ACAD. SCI. U.S.
EMBL; AF041842; G2921579; -
EMBL; AF036163; G2674177; -
SEQUENCE 397 AA; 44302 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
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GLIAL CELL LINE-DERIVED N
GFRA3.
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01-AUG-1998
01-AUG-1998
GDNF FAMILY
SEQUENCE FROM N.A.

BALOH R.H., GORDDINSKY A., GOLDEN J.P., TANSEY POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.; PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).

EMBL; AF051767; G2961632; -.

SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;
                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   060609;
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SUBMITTED
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EUKARYOTA; METAZOA; CHORDATA;
SCIUROGNATHI; MURIDAE; MURINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIDENFALK J.,
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K J., TOMAC A., 1
D (MAR-1998) TO 1
                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL. 07, CREATED)
(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
RECEPTOR ALPHA 3.
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06, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY
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No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
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01-AUG-1998 (TREMBLREL.
GLIAL CELL LINE-DERIVED
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                                                                                                                                                                                                                                                                                                                                                                CVRANELCAAESNCSSRYRTLRQC---LAGR-DRNTMLANKECQAALEVLQESPLYDCRC
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ANCRASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNME
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
NEUROTROPHIC FACTOR RECEF
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53; 1
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Pred. No. 1.23e-158;
78; Mismatches 99;
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015328;
01-JAN-1998
01-JAN-1998
01-NOV-1998
       O35977 PRELIMINARY; PRT; 464 AA.
O35977;
O1-AN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GDNER-BETA OR RETL2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHER
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHR WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., W PEPINSKY R.B., CATE R.L.;
"Glial cell line-derived neurotrophic factor-dependent F can be mediated by two different cell-surface accessory PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
EMBL: U97145; G2282028: -.
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EUKARYOTA; METAZOA; CHORDATA;
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DECEQLEKSFSQNPCLMEAIAA
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1 Similarity 37.3%;
120; Conservation
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98 (TREMBLREL.
98 (TREMBLREL.
D 2.
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Pred. No. 1.23e-158;
78; Mismatches 99;
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LAST SEQUENCE UI
LAST ANNOTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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EUTHERIA:

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RESULT ACCORDED ACCOR
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Best Local S
Matches 12
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015507 PRELIMINARY:
015507;
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
MEDLINE; 97322356.

SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WALUS L., RÓBINSON S., JAWORSKI G., WEI H. PEPTISKY R.B., CATE R.L.; SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ EMBL; AF005226; G2232252; -
EMBL; U97143; G2282024; -
SEQUENCE 464 AA
                                                                                                                                                              TISSUE-KIDNEY
                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                          CATARRHINI; HOMINIDAE;
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CATE R.L.,

"Glial cell line-derived neurotrophic factor-dependent RET activate can be mediated by two different cell-surface accessory proteins."

PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
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MEDLINE; 97322356.
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TRUPP M., RAYNOSCHEK
SUBMITTED (JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN/KIDNEY;
SANICOLA M., HESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVA-PNCLDLRSFCRADPLCRSRLMDFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPDSDLCLKFAMLCTLNDKCDRLRKAYGEACS-GI----RCQRHLCLAQLRSFFEKAAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 25.5%; Smilarity 37.6%; 121; Conservative
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                                                                                                                                                                                                                                            OMOH
                                                                                                                                                                                                                                                                                                                                                               86,03
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EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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74; 1
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Pred. No. 2.44e-157;
                                                                                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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H., TIZARD R.,
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                                                                                                                                                                                                                                                            MAMMALIA;
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                                                                                                                                                                                                                                                         EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHRENFELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RET activation
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                                            PRESULT OF SECOND PROPERTY OF SE
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                                                              SEQUENCE FROM N.A.
STRAIN-C57;
DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF015172; G2624963;
                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
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Match
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Query Match
Best Local S
Matches 12
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                          SEQUENCE FROSTRAIN-C57;
DEY B.K., WO
                                                                                                                                                                                     035252;
DEY B.K., WONG Y.W., TOC
NEUROREPORT 9:0-0(0001).
[2]
                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; V
SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKAGAWARA A.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; U97144; G2282026;
EMBL; U95847; G2459742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISHIKI T., KONDOH K.,
SAKIYAMA S., TAKAHASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SANICOLA M., HESSION C.A., WORLEY D. WALUS L., ROBINSON S., JAWORSKI G., PEPINSKY R.B., CATE R.L., SUBMITTED (APR-1997) TO EMBL/GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROC. NATL. ACAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNYIDSSSLSVAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQA
                                                                                                                                                                                                                                                                                                  A-PNCLDLRSFCRADFLCRSRLMDFQTHCHPMDI-LGTCATEQ-SRCLRAYLGLIGTAMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 37.0%;
128; Conservative
                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 AA;
                                                                                                                                                                                                 PRELIMINARY;
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H., OHNUMA N., TANABE M.,
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                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 744; DB 4; Le
Pred. No. 9.60e-155;
70; Mismatches 126;
                                                                                        VERTEBRATA;
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H., TIZARD R.,
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51134 MW;

910EF17F

CRC32; BB

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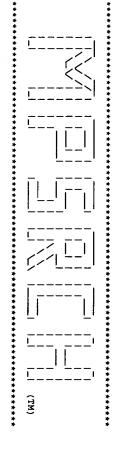
Score

742;

11;

Length

463;



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Mon Mar 8 14:49:21 1999; MasPar time 16.79 Seconds

Run on: Mon Mar 8 14:49:21 1999; MasPar time 16.79 Seconds
480.061 Million cell updates/sec
Tabular output not generated.

Title: >US-08-866-354-43

Description: (1-498) from USO8866354.pep
Perfect Score: 2337
Sequence: 1 MVXXLXXXPXPPPXXXMXLXL.....XLPVLMLTALAXLLSXXXXS 498

Scoring table: PAM 150 Gap 11

Searched: 131922 segs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 32.365; Variance 142.853; scale 0.227

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	8	ID	Description	Pred. No
_	1803	77.2	468	27	W27327	Rat glial cell derive	1.33e-15
2	1803	77.2	468	28	W35334	Rat glial cell line-d	1.33e-15
ω	1803		468	28	W37457	Ret ligand	1.33e-1
4	1788	76.5	464	28	W37460	an Ret Iigan	3.78e-15
տ	1783	76.3	465	28	W35333		1.15e-15
σ	1732	74.1	460	28	W37459	igand 1	1.00e-152
7	1303	55.8	346	28	W37458	ligand	2.70e-111
œ	1030	44.1	400	28	W37463	Ret ligand	4.46e-85
9	982	42.0	397	28	W37461	ligand	1.74e-80
10	866	37.1	346	28	W37465	_	2.05e-69
11	826	35.3	315	28	W37462	Human Ret ligand RetL	1.31e-6
12	96	4.1	1251	14	R79475		1.42e+0
13	93	4.0	469	20	W03448	Farnesoid-activated r	2.32e+01
14	93	4.0	1480	ű	R25079	Drosophila SLIT prote	2.32e+01
15	92	3.9	383	10	R56166	Neuroendocrine tumor	2.73e+0
16	92	3.9	833	σ	R28960	Delta D11.	2.73e+01
17	91	٠ 9.	2189	μ	R05222	Antigen GX5401FL enco	3.20e+01
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W0583	W4429	W4429	W33399	W3339	R9622			R94346				R29928							W37501	0	a	R22461	\mathbf{L}	W03759	R70239	R41920
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			1.55e+02									9.72e+01					Ë	_			Έ.	4.41e+01	L	:	.41e	4.41e+01

ALIGNMENTS

isolated glial cell derived neurotrophic factor receptor alphia useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders Claim 1; Page 78-79; 100pp; English.

This protein comprises full-length rat glial cell derived neurotrophic factor receptor alpha (GDNFR alpha), a novel GPI-linked protein that is a ligand-binding component of the receptor system for GDNF. Its amino acid sequence was deduced from an isolated cDNA clone (see T84975). The invention relates to novel uses of GDNF and its receptor. In particular, it 13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
(GETH) GENENTECH INC.
Klein RD, MOOTE MW, ROSENTHAL A, RYAN WPI; 97-470819/43.
N-PSDB; T84975. Rat glial cell derived neurotrophic factor receptor alpha; GDNFR alpha; GDNF; rat; kidney disease; glomerulonephritis; therapy. W09733912-A2. 18-SEP-1997. Cleavage_site Modified_site Modified_site Modified_site Domain Peptide Key Rattus sp. W27327 standard; Protein; 468 W27327; 27-APR-1998 (first entry) /note= "0-glycosylated" 428..430 /note= "GPI-anchor cleavage/attachment site" /note= "0-glycosylated"
349 25..445 446..468 Location/Qualifiers /note= "0-glycosylated" /note-/note-/label Sig_peptide "extracellular domain" "GPI-attachment site" A ¥

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Best Local :
                                                                                                                                                                                                                                                                                                    treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glaucoma; retinal decentions.
(AMGE-) AMGEN INC.
Fox GM, Jing S, Wen D;
WPI; 97-535836/49.
N-PSDB; T95297.
                                                                                                                                                                                                                                                                                                                                                               Rat; glial cell line-derived neurotrophic fact
Rat; glial cell line-derived neurotrophic fact
treatment; dopaminergic nerve cell disorder;
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                                                                                                    15-APR-1997; U06281
14-APR-1997; US-837199.
22-APR-1996; US-015907.
09-MAY-1996; US-017221.
                                                                                                                                                                                                              WO9740152-A1.
                                                                                                                                                                                                                                                                                       gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W35334 standard; Protein; 468 W35334;
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53.3%;
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Pred. No. 1.33e-159;
23; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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Claim 1; Pages 96-98; 196pp;
The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                            SCSYEXXEKPNCLDLRXXCRTDXLCRSRLADFXTNCXXXXRXVXSCXAXNYXXCLXAYNG
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53.38;
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Pred. No. 1.33e-159;
23; Mismatches 183;
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Parkinson's and
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RESULT 3
ID w37457 standard; Protein; 468 AA.
AC w37457;
DT 21-MAY-1998 (first entry)
DE Rat Ret ligand RetL1.
KW Ret ligand; RetL; RetL1; receptor; signal transduction;
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                                                                                                                                                                                                                                                                                                                                                                                                      CC This protein comprises rat ret ligand (RetL) RetL1, a key component CC of the Ret signalling pathway that specifically interacts with Ret CC receptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain. The amino acid sequence was deduced from a cDNA clone (see V00245) obtained CC from a rat embryonic kidney cDNA expression library. Human RetL1 CC as well as mouse and human RetL2 and RetL3 sequences have also been CC identified (see W37458-63). Vectors containing retL1 DNA and CC identified (see W37458-63). Vectors containing retL1 DNA and CC with these vectors are claimed, as well as a method for production CC proteins with a toxin, imageable compound or radionuclide. RetL1, optionally when expressed from vectors in vivo, is used to promote CC growth of new tissue and survival of damaged tissue, particularly CC kidney or neural tissue. Typical applications are in renal failure, neurodegeneration, motor neurone disease, multiple sclerosis, compounties, kadney transplants, toxic or hypoxic injury. CC sasociated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nerveus cystem (Lyme disease, muscular dystrophy and myasthenia gravis). CC Fusion proteins are used to deliver toxins etc. to Ret-expressing CC cells, especially tumours.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Claim 2; Page 49-51; 113pp; English.
Claim 2; Page 49-51; 113pp; English.
This protein comprises rat Ret ligar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
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                                                                                                                                                       IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXP
                          itpcttsmsn-evcnrrkchkalrqffdkvpakhsygmlfcscr--diacterrrqtivp
                                                                               LEXSPYEPXVTSRLSDIFRXXSXXSXXXXXXXXXXKSNXCLDAAKACNLNDXCKKLRSAY
                                                                                                    ledspyep-vnsrlsdifravpfisdvfqqvehiskgnncldaakacnlddtckkyrsay
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255; Conser
                                                                                                                                                                                                                                                                                                                                                                                            468 AA;
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53.38;
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Pred.
23; M
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Mismatches 183;
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            principle (cells)

Principle (cells)

Claim 2; Page 69-70; 113pp; English.

Claim 2; Page 69-70; 113pp; English.

Chaim 2; Page 69-70; 113pp; English.

Claim 3; Page 69-70; 113pp; English.

Claim 4; Page 69-70; 113pp; English.

Claim 4; Page 69-70; 113pp; English.

Claim 4; Page 69-70; 113pp; English.

Claim 5; Page 69-70; 113pp; Engl
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
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WO9744356-A2.
27-NOV-1997.
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Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
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Treat dopaminergic nerve cell disorders, e.g. Parkinson's and Treat dopaminergic nerve cell disorders, e.g. Parkinson's and Treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's Claim 1; Pages 91-93; 196pp; English.

The present sequence is the human glial cell line-derived neurotrophic factor (GDNF) receptor, which can be used to treat Copaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's Colsease or amyotrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) Colsease or amyotrophic lateral sclerosis, combination with GDNF) Colsease or amyotrophic lateral sclerosis, combination with GDNF) Colsease and the receptor can also be used to block Colsease are sensory neurons. The receptor can also be used to block Conwanted GDNF activity, analyse GDNF related molecules and Stabilise GDNF in pharmaceutical formulations. Receptor expressing cells, preferably transfected ex vivo, can be used similarly by is implantation, and the use of the receptor CDNA in gene therapy is
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Best Local Similarity
Matches 262; Consei
                                                                                                                                                                                                                                                                                             15-APR-1997; U06281.

14-APR-1997; US-837199.

22-APR-1996; US-015907.

09-MAY-1996; US-017221.

(AMGE-) AMGEN INC.

FOX GEN INC.
                                                                                                                                                                                                                                                        Glial cell line derived neurotrophic factor receptor - use treat dopaminergic nerve cell disorders, e.g. Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human glial cell line-derived neurotrophic factor receptor. Human; glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzhelmer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glaucoma; retinal degeneration; hearing loss;
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W35333 standard; Protein;
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17; Mismatches 166;
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21-MAY-1998 (first entry)
Human Ret ligand RetL1.
RetL1; receptor; signal transduction; human Ret ligand; RetL1; receptor; signal transduction; human cell growth; renal cell; nerve cell; renal failure; nephritis kidney transplant; toxic injury; hypoxic injury; heurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;

nephritis;

Homo sapiens. W09744356-A2. myasthenia gravis;

tumour;

therapy

W37459 standard; W37459;

Protein;

460

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Mar 8 14:52:02 1999; MasPar time 24.44 Seconds 763.226 Million cell updates/sec

Run on:

Title:

Description: Perfect Score: Sequence: >US-08-866-354-43 (1-498) from USO8866354.pep 2337 1 MYXXLXXXPXPPXXXMXLXL.....XLPVLMLTALAXLLSXXXXS 498

Scoring table: PAM 150 Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 43.709; Variance 79.332; scale 0.551

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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99999999999999999999999999999999999999	Score
	Query Match
397 493 2524 3071 3071 1121 3071 3071 427 1251 469 1460 2540 2540 200 2540 2540 2540 2540 2540	Length
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GPI-linked receptor - epidermal growth fact Xotch protein - Afric Xotch protein - Afric fibrillin precursor fibrillin precursor fibrillin protein - human hypothetical protein extracellular protein phoc protein precurso latent transforming farnesoid x-activated epidermal growth fact DL receptor precurso slit protein precur slit protein precur notch protein precur notch protein homolog hypothetical 11.6K pr hypothetical 11.6K pr fetal antigen homo fetal antigen homo fetal antigen bould serum albumin - builf	Description
7.35e-03 7.35e-03 7.35e-02 2.04e-02 2.83e-01 3.89e-01 3.89e-01 9.98e-01 9.98e-01 9.98e-01 1.36e+00 1.36e+00 2.51e+00 2.51e+00	Pred. No.

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cell-fate determining	tenascin precursor -		Balbiani ring 3 prote	chitin synthase (EC 2	LDL receptor precurso	₩,	activin type I recept	preadipocyte factor 1	gasl protein - mouse	hypothetical protein	fibrillin-2 precursor	fibrillin-2 precursor	notch protein homolog	cobalamin biosynthesi		gene Delta protein pr	neurogenic protein De	monocyte surface anti	hemagglutinin-neurami	delta-like dlk homeot	homeotic protein dlk
•		9.55 E.S.	3.34	3.300.00	3.390:00	3.39e+00	3.39c+00	4.57e+00	4.57e+00	3.39e+00	1.36e+00	1.36e+00	2.51e+00	1.85e+00	1.36e+00	1.36e+00	1.36e+00	1.85e+00	2.51e+00	1.36e+00	1.36e+00

ALIGNMENTS

Db 169 HDKCD : Cy 185 NDXCK	Db 117 VHPAR 1 Qy 125 XHXXL	Db 60 HLGSC Oy 65 TLRQC	Db 3.LSWSP Qy 5.LXXXP	Query Match Best Local Si Matches 157	SUMMARY	380-397 92,145,306	KEYWORDS FEATURE	#cross-r COMMENT This	##molecule	#accession	#journal #title	#authors	ACCESSIONS REFERENCE	ORGANISM DATE	TITLE ALTERNATE NAMES	RESULT 1
HDKCDRLRKAYGEACSGI-RCORHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAG 223 : :	VHPARSIGDYELDVSPYEDTVTSK-PWKM-NL-SKLNMLKPD-SDLCLKFAMLCTL 168	HLGSCTSSLSRPLPL-EESAMSADCLEAAEQLRNSSLIDCRCHRRWKHQATCLDIYWT 116	LSWSPRPPLL-MIL-LLVLSLWLPLG-AGNSLATENRFVNSCTQARKKCEANPACKAAYQ 59	y Match 42.0%; Score 982; DB 2; Length 397; Local Similarity 37.6%; Pred. No. 4.74e-190; hes 157; Conservative 41; Mismatches 194; Indels 26; Gaps 19;	#length 397 #molecular-weight 44307 #checksum 2962	# action by the carbohydrate (Asn) (covalent) # status # binding_site carbohydrate (Asn) (covalent) # status	glycoprotein	#cross-references DDBJ:AB008833; NID:g2627159; PID:g2627160 This protein plays a distinct role in cell survival and differentiation.	#molecule_type mRNA #residues 1-397 ##label NOM	novel cDNA related to GDNFRalpha and NTNRalpha. ${\tt JE0082}$	Biochem. Biophys. Res. Commun. (1998) 244:849-853 Molecular cloning and expression analysis of GFRalpha-3.8	Nomoto, S.; Ito, S.; Yang, L.X.; Kluchi, K.	JE0082 JE0082	#formal_name Mus musculus #common_name house mouse 21-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1998	GPI-11nked receptor - mouse GFRalbha-3	JEOORS #type complete

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KEYWORDS
FEATURE
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REFERENCE
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200-237,238-277,
278-318,319-359
249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.6%;
Best Local Similarity 17.5%;
                                                                                                                                                                                                                #journal #title
                                                                                                                                                                          #accession
                                                                                                                                                                                              #cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession
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                                                                                                ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-493 ##label OZA
##cross-references DDBJ:D89730; NID:g2429082; PID:d1023127; PID:g2429083
This protein plays a role in the regulation of cell growth by
interacting with DAN protein through DA41 protein.
                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 RIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQVCINLRGSFTCHCLPGYQKRGEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RXXSXXSXXXXXXXXXXXXXXSNXCLDAAKACNLNDXCKKLRSAYIXXCXXXX-SXXERC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYXXCLXAYXGLIGTXMTPNYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-SRCLRAYLGLIGTAMTPNFI--SKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGERRRUTIAPSCALPSV-TPNCLDLRSFCRADPLCRSRLMDFQTHCHPMD-ILGTCATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                      #superfamily unassigned ankyrin repeat proteins;
repeat homology; EGF homology
                                                                                                                                                                                      COffman, C.; Harris, W.; Kintner, C. Science (1990) 249:1438-1441 Xotch, the Xenopus homolog of Drosophila nces_MUID:90385285
                                         transmembrane protein
                                                                                                                                                                          A35844
                                                                                                                                                                                                                                                                                                                         #159844 #type complete
Xotch protein - African clawed frog
Xotch protein - African clawed frog
#formal_name Xenopus laevis #common_name African clawed
12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. (1997) 237:245-250 Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5).
                                                                                                                                                                                                                                                                     A35844
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epidermal growth factor-like protein, T16 - rat
#formal_name Rattus norvegicus #common_name Norway rat
09-Oct-1997_#sequence_revision 07-Nov-1997 #text_change
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                                                                                                1-2524 ##label COF
                                                                                                                                   preliminary; nucleic acid sequence not shown; compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #region epidermal growth factor-like repeat\
#binding_site carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain signal sequence #status predicted #label SIG
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h 493 #mo
EGF homology
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Pred. No. 7.35e-03;
12; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.; Nakamura, Y.; Ichimiya,
     #label
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1957-1989
1991-2023
2024-2056
2057-2089
                                                                          #authors
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                                                                                                                                                                                                                                                                                                            2028 -TCSNTEGSFKCLCPEGFSWSSS-GRR-CQ-DLRMSY 2060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1150 SPNPCQNGATCTDYLGGYSCECVAGYHGVNC-SEEINECLSHPCQNGGTCIDLINTYKCS 1208
                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1264 CEGD-VNECLSNPCDSRGTQNCIQLVNDYRCECRQGFTGR-RCE 1305
                                                                                                                                                                                                                                                                             186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
##residues 1-2871 ##label YIN
##cross-references GB:L29454; NID:g575509; PID:g575510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                             DXCKKLRSAYIXXCXXXXSXXERCNRRKCHKALRQFF
                                                                                                                                                                                                                                                                                                                                                CKRGMKKEXXCLXIYWSXHXXLXXGNXXLEXSPYEPX-VTSRLSDIFRXXSXXSXXXXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXKSNXCLDAAKACNLNDXCKKLRSAYIXXCXXXXXXXXERCN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AXXXCXAEXXCSXXYRTLR-QCXAGXXXNTXLASGXEXXXXXXXXXXXXXXXXXXSSLYDCR 107
                                                                                                                                                                                                                                                                                                                                                                                                                     4.5%;
Similarity 15.5%;
15; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 4.6%;
Similarity 15.2%;
25; Conservative
                Sakai, L.Y.
Genomics (1993) 17:476-484
Fibrillin binds calcium an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yin, W.; Smiley, E.; Germiller, J.; Sanguineti, T.; Pereira, L.; Ramirez, F.; Bonadio, J. J. Biol. Chem. (1995) 270:1798-1806
Primary structure and developmental expression of mouse fibrillin gene.
                                                                                                                                              #formal_name Homo sapiens #common_name man 02-Jun-1995 #sequence_revision 25-Apr-1997
                                                                        Corson, G.M.; Chalberg, S.C.;
                                                                                                            A47221; I54355; S17064; I59574; S17062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #55624 #type complete
fibrillin-1 precursor - mouse
#formal_name Mus musculus #common_name house mouse
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                                 A47221 #type fragment
f1br1ll1n 1 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A55624
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#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN3\
#domain ankyrin repeat homology #label AN4\
#domain ankyrin repeat homology #label AN5
#domain ankyrin repeat homology #label AN5
#domain ankyrin repeat homology #label AN5
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   multidomain structure and
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105; DB 2; Le
Pred. No. 2.04e-02;
N1smatches 59;
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Pred. No. 7.35e-03;
21; Mismatches 108;
is coded by cDNAs that reveal alternatively spliced exons at
                                                                        Dietz,
                                                                                                                                                                                                                                                                             222
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                                                                        H.C.; Charbonneau,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:55:25 1999; MasPar time 37.44 Seconds 733.893 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-866-354-43 (1-498) from US08866354.pep 2337

1 MVXXLXXXPXPPXXXXXXLXL.....XLPVLMLTALAXLLSXXXXXS 498

Scoring table: PAM 150 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb18

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 43.734; Variance 73.928; scale 0.592

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	8	Ħ	Description	Pred. No.
1	1788	76.5	464	4	015316	GLIAL CELL LINE-DERIVE	0.00e+00
N	1788	76.5	464	4	015328	RET LIGAND 2.	0.00e+00
ω	1786	76.4	464	11	035977	GLIAL CELL LINE-DERIVE	0.00e+00
4	1783	76.3	465	4	043912 .	GPI-LINKED ANCHOR PROT	0.00e+00
Ç	1778	76.1	468	11	035246	GDNF RECEPTOR ALPHA.	0.00e+00
σ	1752	75.0	463	11	035748	GDNFR-ALPHA/TRNR1-DELT	0.00e+00
7	1732	74.1	460	4	015507	RET LIGAND 1.	0.00e+00
œ	1727	73.9	463	11	035252	GDNF RECEPTOR BETA.	0.00e+00
9	1218		431	13	093512	GFR RECEPTOR ALPHA 4 P	2.58e-262
10	1027	43.9	400	4	060609	GDNF FAMILY RECEPTOR A	4.39e-215
片	982	42.0	397	11	055243	GLIAL CELL LINE-DERIVE	5.26e-204
12	982	42.0	397	11	035118	GLIAL CELL LINE DERIVE	5.26e-204
13	982	42.0	397	11	035325	GLIAL CELL LINE-DERIVE	5.26e-204
14	110	4.7	1523	11	088280	MEGF5.	1.96e-03
15	108	4.6	493	11	035568	T16.	4.09e-03
16	106	4.5	1451	u	Q20538	SIMILAR TO MATRIN F/G.	8.48e-03
17	104	4.5	3857	Ľ	088840	MUTANT FIBRILLIN-1.	1.74e-02
18	101	4.3	739	4	075094	MEGF5 (FRAGMENT).	5.06e-02
19	97	4.2	192	ហ	001471	COSMID CO4E6.	2.03e-01
20	97	4.2	1095	4	Q99458	NOTCH4 (FRAGMENT).	2.03e-01

45	44	43	42	41	40	39	38 8	37	36	35	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21
92	92	91	92	91	90	91	91	92	92	90	91	94	93	93	93	95	96	96	99	97	97	97	99	97
3.9	3.9	3.9	3. 9	3. 9	3.9	3.9	3.9	3.9	3. 9	٠ 9	3.9	4.0	0	4.0	4.0	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2
3507	2352	1890	1706	1698	1687	1253	1232	1077	832	817	271	1722	733	530	469	2018	1062	387	2531	2003	1999	1964	1127	1121
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Q23587	061240	049528	042900	Q9443B	Q61204	Q61810	Q58318	074853	099108	014592	081111	Q19350	Q25678	Q24526	Q62735	Q20487	Q60789	Q12805	016004	000306	Q99940	035442	Q94248	78868D
CODED FOR BY C. ELEGAN	HRNOTCH PROTEIN.	GENE 11-1 PROTEIN - LI	PROTEIN KINASE.	185 KDA SILK PROTEIN.	NOTCH2-LIKE (EGF REPEA	LATENT TRANSFORMING GR	HYPOTHETICAL PROTEIN M	PUTATIVE CYSTINE-RICH	NEUROGENIC LOCUS DELTA	COMP_HUMAN.	RECEPTOR-LIKE KINASE (SIMILAR TO EGF-LIKE RE	FIBRILLIN (FRAGMENT).	SLIT LOCUS ENCODING A	FARNESOID X ACTIVATED	SIMILAR TO RAT TRG GEN	FIBRILLIN-2 (FRAGMENT)	EXTRACELLULAR PROTEIN	NOTCH HOMOLOG.	NOTCH4.	NOTCH4.	NOTCH4.	CODED FOR BY C. ELEGAN	(HHV-6).
1.090.0	1.090-11.	1.51e	1.0%	1.51000	2.04	1.515.	1.51.	1.03	1.0%	0	1.5	5.600	7.81 .	7.83/	7.82	4.000	2.850-1	2.85e-0	1.02ຕ-0		2.03e-0	.03e	1.02e-01	2.03e-01

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	248 KPNCLDLRGYCRTDHLCRSRLADFHANCRASYQTYTSCPADNYQACLGSYAGMIGFDMTP 307	204 SXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEXXE 263	190 SPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYEDKE 247	144 XVTSRLSDIFRXXSXXXXXXXXXXXXXXXXXXCLDAAKACNLNDXCKKLRSAYIXXCXXXX 203	131 -VTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREI 189	84 EXXXXXXCXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGNXXLEXSPYEP 143	-22	24 ALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXXNTXLASGX 83	19 SLASPSSLQGPELHGW-RPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRNTMLAN-K 76	Query Match 76.5%; Score 1788; DB 4; Length 464; Best Local Similarity 56.2%; Pred. No. 0.00e+00; Matches 262; Conservative 17; Mismatches 166; Indels 21; Gaps 9;	SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;	SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EVET. HOSZOS. COJSTST.	WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,	SEQUENCE FROM N.A. TISSUE-FETAL BRAIN:	Ξ	EUNARIOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; FRIMATES; CATARRHINI; HOMINIDAE; HOMO.	IS (HUMAN)	GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.	TREMBLREL.	1998 (TREMBLREL. 05,	LT 1 015316 PRELIMINARY; PRT; 464 AA.

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01-JAN-1998
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RET LIGAND 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Local Similarity 56.2%;
hes 262; Conservative
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                                                SMCFTELTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLKLAL 464
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XXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLT-AL
                                                                                                   NYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGXXXXXXXXX
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Pred. No. 0.00e+00;
17; Mismatches 166;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMATES
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RESULT

ID O35977;
AC O35977;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DT 01-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN CDNER-BETA OR RETL2.

OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODE
SCIURGUNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RC SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
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"Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.":

PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
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                                 SMCFTELTTNISPGSKKVIKLNSGSSRARLSAALTALPLLMLTLAL
                                                                                                        XXPXFSVXXXXXTXTXAXRVXXXPSLXXXXXSXXXXXLXTXVXXXXCXXLQXQXLKXNXSXEX
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     XXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLT-AL
                                                                                                                                                                                                                      NYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGXXXXXXXXX
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Similarity 56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 0.0
19; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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     488
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SHEFELBANE S.E., KHORANA S., SCHULTZ P.N., HU
FOX G.M., JING S., COTE G.J., GAGEL R.F.;
HUM. GENET. 0.0-0(1998).

EMBL; AF038411; G2921545; JOINED.
EMBL; AF038413; G2921545; JOINED.
EMBL; AF038414; G2921545; JOINED.
EMBL; AF038415; G2921545; JOINED.
EMBL; AF038416; G2921545; JOINED.
EMBL; AF038416; G2921545; JOINED.
EMBL; AF038417; G2921545; JOINED.
EMBL; AF038418; G2921545; JOINED.
EMBL; AF038419; G2901557; --
EMBL; AF038419; G2901557; --
EMBL; AF038490; G3068783; JOINED.
EMBL; AF058990; G3068783; JOINED.
EMBL; AF058991; G3068783; JOINED.
EMBL; AF058992; G3068783; JOINED.
EMBL; AF058994; G3068783; JOINED.
EMBL; AF058995; G3068783; JOINED.
EMBL; AF058996; G3068783; JOIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ULT 4
043912 PRELIMINARY;
043912;
01-JUN-1998 (TREMBLREL 06, C)
01-JUN-1998 (TREMBLREL 06, C)
01-AUG-1998 (TREMBLREL 07, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGRIST M., JING S., BOLK FOX G.M., CHAKRAVARTI A.; GENOMICS 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFRA1.
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                       292
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LIGTVMTPNYIDSS-SLS-VAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGS
                                                                                                                                                                                                                                                     LEDSPYEP-VNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAY 174
                                                                                                                                                                                                                                                                                                                                                                                            MXLXLLSLALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXXRTLRQCXAGXXX 75
                                                                                                                                                                                                                                                                                                                                                                                                                     MFLATLYFALPLLDLLLSAEVSGGDRL--DCVKASDQCLKEQSCSTKYRTLRQCVAGKET
                                                                                     VCSYEEREKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSG
                                                                                                                                                                    ITPCTTSVSN-DVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCR--DIACTERRRQTIVP
                                                                                                                                                                                                                              NTXLASGXEXXXXXXXXXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGNXX 135
                                                                                                                                                                                                                                                                                                                                    NFSLASGLEAKDE--CRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDL 115
                                                             IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255;
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larity 52.8%;
Conservative
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Pred. No. 0.00e+00;
25; Mismatches 185;
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1C4EAE03 CRC32;
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035246; PRELIMINARY;
035246; (TREMBLREL 0
01-JAN-1998 (TREMBLREL 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF014117; G2624961; -.
SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO
NEUROREPORT 9:0-0(0001).
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                          404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 76.1%;
Local Similarity 52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFLATLYFYLPLLDLLMSAEVSGGDRL--DCVKASDQCLKEQSCSTKYRTLRQCVAGKET
KSNVSGSTHLCLSDNDYGKDGLAGASSHITTKSMAAPPSCGLSSLPVMVFTALAALLS
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                                                                                                                                                                    SCSYEXXEKPNCLDLRXXCRTDXLCRSRLADFXINCXXXXRXVXSCXAXNYXXCLXAYXG
                                                                                                                                                                                                                                                                                                       VCSYEERERPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEXSPYEPXVTSRLSDIFRXXSXXSXXXXXXXXXXXXXCLDAAKACNLNDXCKKLRSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEDSPYEP-VNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFSLTSGLEAKDE--CRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MXLXLLSLALPLXXXLQGAELXGXXRLXXDCVXAXXXCXAEXXCSXXYRTLRQCXAGXXX
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                                                                         DVTMWQPA--P--PVQTTTATTTTAFRIKNKP-LGPAGSENE-IPTHVLPPCANLQAQKL 403
                                                                                                                                                                                                                                                                                                                                                                           IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTLX
                                                                                                                                                                                                                                                                                                                                                                                                        ITPCTTSMSN-EVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCR--DVACTERRRQTIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTXLASGXEXXXXXXCXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGNXX 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KXNXSXEXXXCFXELTTNXXXXSGXXXXIXXXSXXAXPSXALXXLPVLMLTALAXLLSXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1778; DB 11;
Pred. No. 0.00e+00;
29; Mismatches 183
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                       461
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EHRENFELS C., WHITTY A.,

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RESULT OF STREET OF STREET
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D 035748;
PRELIMINARY;
PRT; 463 AA.
C 035748;
T 01-JAN-1998 (TREMBLREL. 05, CREATED)
T 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
T 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
T 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GDNFA-ALPHA/TRNN1-DELTA PROTEIN.
DE GDNFA-ALPHA/TRNN1-DELTA PROTEIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUT
CC SCTTROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                             O15507 PRELIMINARY;
O15507;
O1-JAN-1998 (TREMBLREL. C
O1-JAN-1998 (TREMBLREL. C
O1-NOV-1998 (TREMBLREL. C
RET LIGAND 1.
              TISSUE-KIDNEY;
MEDLINE; 97322356
                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHONG J., ANNIES M., HEUMANN R.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-HANNOVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVTMWQPA--P--PVQTTTATTTTAFRVKNKP-LGPAGSENE-IPTHVLPPCANLQAQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGTXMTPNYVDSSXTXXXVAPWCXCRGSGNXXEECEKFLXFFXXNPCLXNAIQAFGNGX 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCSYEXXEKPNCLDLRXXCRTDXLCRSRLADFXTNCXXXXRXVXSCXAXNYXXCLXAYXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCSYEERERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KXNXSXEXXXCFXELTTNXXXXSGXXXXXIXXXSXXAXPSXALXXLPVLMLTALAXLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFSLTSGLEAKDE--CRSAMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDL
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larity 53.3%;
Conservative
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 0.00e+00;
23; Mismatches 178;
                                                                                                                                            VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                              460
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                                                                                                                                            EUTHERIA;
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Best Local Similarity 52.8%;
Matches 255; Conservative
                      ULT 8
035252 PRELIMINARY;
035252;
01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKAGAWARA A.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; U97144; G2282026; -
EMBL; U95847; G2459742; -
SEQUENCE 460 AA; 50838 MW; 022FFECA CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-SUBSTANTIA NIGRA;
HISHIKI T., KONDOH K., ICHI
SAKIYAMA S., TAKAHASHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANICOLA M., HESSION C.A., WORLEY D. WALUS L., ROBINSON S., JAWORSKI G., PEPINSKY R.B., CATE R.L.; SUBMITTED (APR-1997) TO EMBL/GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHI WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WEINSKY R.B., CATE R.L.;
"Glial cell line-derived neurotrophic factor-dependent F can be mediated by two different cell-surface accessory PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
                                                                                                                                                                                                                                                                          496 XXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGTVMTPNYIDSS-SLS-VAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGS 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEDSPYEP-VNSRLSDIFRVVPFISV---EHIP--KGNNCLDAAKACNLDDICKKYRSAY 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXP
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                                                     88,8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GENBANK/DDBJ
                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 0.00e+00;
25; Mismatches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .S.,
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H., TIZARD
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                                               UPDATE)
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Length 460; Indels

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Gaps

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                                                                                                                                                                                                                                                                  O93512 PRELIMINARY; PRT; 431 AA.
093512;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GFR RECEPTOR ALPHA 4 PRECURSOR.
GALLUS (CHICKEN).
GALLUS (CHICKEN).
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DEY B.K., WONG Y.W., TOO
NEUROREPORT 9:0-0(0001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL, AF015172; G2624963; -.,
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                            THOMPSON J., DOXAKIS E., PINON L.G., STRACHAN WYATT S., BUCHMAN V.L., DAVIES A.M.;
"GFRAlpha-4, a new GDNF family receptor.";
MOL. CELL. NEUROSCI. 11:117-126(1998).
EMBL; AF045162; G2906032; -.
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                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 98313402.
                                                                                                                                                                                                                                                NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE;
  SIGNAL
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Pred. No. 0.00e+00;
29; Mismatches 178; Indels 22;
POTENTIAL
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SEQUENCE
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EMBL; AF051167; G2961632; -.
SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
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NDRGCGERRRNTIAPNCALPPVA-PNCLELRRLCFSDPLCRSRLVDFQTHCHPMD-ILGT | :| | | | | | | | | :| :: : :
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                                                                            ACNINDXCKKIRSAYIXXCXXXXXXXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXX 240
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l Similarity 45.9%;
157; Conserva+4
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47964 MW;
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Pred. No. 2.58e-262;
39; Mismatches 132;
                                                                                                        -SGP-HCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAP
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055243;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TOMAC A., 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
MIRIDAE; MURINAE; MUS.
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01-JUN-1998 (TREMBLREL.
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l Similarity 37.6%;
157; Conservative
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  PRELIMINARY;
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06, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY
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Pred. No. 5.26e-204;
41; Mismatches 194;
 PRT;
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O1-JAN-1998 (TREMBLREL O5, CREATED)
O1-JAN-1998 (TREMBLREL O5, LAST SEQUENCE UPI
O1-NOV-1998 (TREMBLREL O8, LAST ANNOTATION (
GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR |
(GFRALPHA-3),
(GFRALPHA-3),
GFRAJORA-3,
GFRAJORA-3,
GUS MUSCULUS (MOUSE),
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAI
SCLUROGNATHI; MURIDAE; MURINAE; MUS.
                                 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIC
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTO
GFRA-3.
MUS MUSCULUS (MOUSE).
EUKARROTA; METAROA; CHORDATA; VERTEBRATA;
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035325;
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NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;

"MOLECULAR cloning and expression analysis of GF
CDNA related to GDNFR alpha and NTNR alpha.";
BIOCHEM. BIOPHYS. RES. COMMUN. 244:849-853(1998)
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l Similarity 37.6%;
157; Conservative
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                                                                                                            05, CREATED)
05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
NEUROTROPHIC FACTOR FAMIL
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05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA
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Pred. No. 5.7
41; Mismatch
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1. No. 5.26e-204;
Mismatches 194;
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Best Local S
Matches 15
                                                                                                                                                                                                                      C STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;

MEDLINE; 98360089.

A NAKAYAMA M., NAKAJIMA D., NAGASE T., NOMURA N., SEKI N., OHA

"Identification of high-molecular-weight proteins with multi
EGF-like motifs by motif-trap screening.";

GENOMICS 51:27-34(1998).

R EMBL; ABO11531; D1033424; -.

R PROSITE; PS01185; CTCK_1; 1.

R PROSITE; PS01186; EGF_2; 7.

R PROSITE; PS01186; EGF_2; 7.

R PROSITE; PS01187; EGF_CA; 2.

GLYCOPROTEIN; EGF-LIKE DOMAIN.

SEQUENCE 1523 AA; 167767 MW; 2BD845D0 CRC32;
                                                                                                                 Matches
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088280;
01.NOV-1998 (TREMBLREL. 08, C:
01-NOV-1998 (TREMBLREL. 08, L.
01.NOV-1998 (TREMBLREL. 08, L.
MEGF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; MORIDAE; MURIDAE; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;

SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS

EMBL; AF020305; G2429367; -.

SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;
                                                     1038 CVPEMNLCQHEAKCISLDKGFRCECVPGYSGKLC-ETDNDDCVAHKCRHGAQCVDAVNGY 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEGF 5
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  46
                                                                                                           / Match 4.7%;
Local Similarity 19.4%;
les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDKCDRLRKAYGEAC----SGI-RCQRHLCLAQLRSFFEKAAESHAQGLLLCPCPPEDAG
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  CVXAXXXCXAEXXCSXXYRTLR-QCXAGXXXNTXLASGXEXXXXXXCXXAXEXLXXSSLY 104
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44333 MW; F0C0C841 CRC32;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 5.26e-204;
41; Mismatches 194;
                                                                                                           Score 110; DB 11; Pred. No. 1.96e-03; 12; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1523
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RATTUS.
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Matches 1
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035568;
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01-JAN-1998
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EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODEN";\:
COTHROGNATHI: MURIDAE; MURINAE; RATTUS.
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PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 6.
PFAM; PF00008; EGF; 3.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 493 AA; 54596 MW; 913;
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BIOCHEM. BIOPHYS. RES. COMMUN.
EMBL; D89730; D1023127; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OZAKI T., KONDO K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97415782.
                                                                                                                                     154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interaction of DA41, a DAN-binding protein, with the epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCICPQG 1103
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                                                                                                                                  RXXSXXSXXXXDXXXXXKSNXCLDAAKACNLNDXCKKLRSAYIXXCXXXX-SXXERC
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Similarity 17.5%;
10; Conservative
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(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
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                               œ
                               14:58:05 1999
                                                                                                                                                                                                                                                                Score 108; DB 11;
Pred. No. 4.09e-03;
12; Mismatches 34;
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd **-**

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output Run on: not generated Mon Mar 8 15:02:15 1999; MasPar time 16.42 Seconds 481.862 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-866-354-44 (1-489) from US08866354.pep

2092 1 XX XXXXXXXXXPXXXXLXTLXS.....PVLMLTXLXXXLXXXLXETS

Scoring table: PAM Gap 1150

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: 31.576; Variance 131.408; scale 0.240

score and is Pred. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

11 22 33 34 34 34 34 34 34 34 34 34 34 34 34	Result
1779 1779 1779 1768 1695 1695 1695 1799 976 976 977 977 9861 987 988	Score
4444 6788888 8888 8555 8555 8555 8555 8555 8	% Query Match
468 468 464 464 467 460 346 397 460 315 183 383 383 383 383 383 383 469 443 383 686	Length
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Rat glial cell derive Rat glial cell line-d Rat Ret ligand RetLI. Human Ret ligand RetLI Mouse Ret ligand RetLI Mouse Ret ligand RetLI Mouse Ret ligand RetLI Chicken cytotactin. Neuroendoctine tumor Farnesoid-activated rasking protein high Neuroendoctine tumor Human extracellular/e Human alpha meltrin p	Description
2.89e 167 2.89e 167 2.89e 166 3.90e 166 1.23e 158 2.11e 153 1.41e 113 3.53e 85 1.55e 73 2.81e 67 7.49e+01 1.49e+01 1.49e+01 1.49e+01 1.55e+01 2.51e+01 3.51e+01 3.51e+01 3.51e+01	Pred. No.

14 R79475 Mouse alpha meltri 14 R79475 Mouse LTBP-3, 3 R10872 Protein encoded by 6 R28960 Delta Dil. 5 R28960 Delta Dil. 5 R25079 Drosophila SLIT pi 1 R05222 Antigen GX5401FL 6 28 W25720 Adhesive protein. 6 R29928 Eimeria antigen EX 16 R94346 Hepatitis GB virus 3 R13757 Prolactin. 18 W33398 Human haematopoiet 28 W33398 Human nel-related 28 W33398 Human nel-related 28 W33398 Human nel-related 29 R47850 Human DL recepton 9 R47856 Human DL recepton 9 R47850 Human LDL recepton 10 R78234 Amino acid sequenc 11 R94562 Human alpha-2-MR. 11 R94561 Human alpha-2-MR. 12 R47861 Alpha 2-Macroglobb 25 W18352 Proliferation and								38 79																			
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	iferation and d	2-Macroglobul	Human alpha-2-MR.	Human cytotactin.	chimeric	chimeric	sequenc	P95/human	human	LDL receptor	LDL receptor	membrane prote	_		ö	matopoieti	Prolactin.	_	ntigen Eaml	protein.	Ľ.	401FL	SLIT prot		oded by	LTBP-3.	alpha meltrin

ALIGNMENTS

RESULA

NOTICE PROPERTY OF THE TENT OF THE PN W09733912-A2.

PD 18-SEP-1997; U04363.

PF 13-MAR-1996; US-618236.

PR 14-MAR-1996; US-618236.

PR 14-MAR-1996; US-618202.

PR 14-MAR-1996; US-618202.

PR 14-MAR-1996; US-615902.

PR (SETH) GENENTECH INC.

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PR WPI; 97-470819/43.

PR N-95DB; T84975.

PR N-95DB; T84975.

PR WPI; 97-470819/43.

PR N-95DB; T84975.

PR Isolated glial cell derived neurotrophic factor receptor alpha
PT useful to develop products to diagnose and treat associated

disorders, particularly enteric nervous system or kidney disorders

PS Claim 1; Page 78-79; 100pp; English.

CC This protein comprises full-length rat glial cell derived

CC This protein comprises full-length rat glial cell derived

CC GPI-linked protein that is a ligand-binding component of the

CC GPI-linked protein that is a ligand-binding component of the

CC GPI-linked protein comprises full-length rat glial cell derived

CC GPI-linked protein that is a ligand-binding component of the

CC GPI-linked protein component of the

CC GPI-linked protein that is a ligand-binding component of the

CC This protein comp W27327; 27-APR-1998 (first entry) Rat glial cell derived neurotrophic factor receptor alpha; Glial cell derived neurotrophic factor receptor alpha; GDNF; rat; kidney disease; glomerulonephritis; therapy. JT 1 W27327 standard; Protein; 468 AA. Cleavage_site Modified_site Modified_site Domain Domain Key Rattus sp. Modified_site Peptide 428..430 /note= "G /note= "0-glycosylated"
349 446..468 Location/Qualifiers /note= "0-glycosylated" 'note= "0-glycosylated" /note-/note-/label Sig_peptide "GPI-anchor cleavage/attachment site" "extracellular domain" "GPI-attachment site" GDNFR alpha:

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W09740152-A1.

30-OCT-1997.

15-APR-1997; U05281.

14-APR-1997; US-837199.

22-APR-1996; US-015907.

09-MAY-1996; US-017221.
      (AMGE-) AMGEN INC.
FOX GM, Jing S, Wen D;
WPI; 97-535836/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to native rat GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antibodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNF, diagnostic techniques for identifying GDNF-related conditions, methods for identifying molecules homologous to GDNFR alpha, and therapeutic techniques (claimed) for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system
                                                                                                                                                                                                 Rat; glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
                                                                                                                                                                                     Huntington's disease;
                                                                                                                                                                                                                                               Rat glial cell
                                                                                                                                                                                                                                                                  01-MAY-1998
                                                                                                                                                                                                                                                                                 W35334;
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                                                                                                                                                                   therapy.
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                                                                                                                                                                                                                                                line-derived neurotrophic factor receptor.
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                                                                                                                                                                                    glaucoma;
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Pred. No. 2.
12; Mismatc
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2.89e-167;
ches 213;
                                                                                                                                                                                degeneration; hearing loss;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glial cell line derived neurotrophic factor receptor - utreat dopaminergic nerve cell disorders, e.g. Parkinson' Alzheimer's disease
Claim 1; Pages 96-98; 196pp; English.
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Pred. No. 2.89e-167;
12; Mismatches 213;
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RESULT
ID WI
AC WI
DT 21
DE RE

Rat Ret ligand RetL1

RetL; RetL1; receptor;

signal transduction;

21-MAY-1998 (first entry)

W37457 :

standard;

Protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                             creceptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain. The amino acid sequence was deduced from a cDNA clone (see V00245) obtained from a rat embryonic kidney cDNA expression library. Human RetL1 as well as mouse and human RetL2 and RetL3 sequences have also been identified (see W37458-63). Vectors containing retL1 DNA and prokaryotic or eukaryotic host cells transformed or transfected with these vectors are claimed, as well as a method for production of RetL1, its soluble variants (e.g. mano acids 1-434) and fusion proteins with a toxin, imageable compound or radionuclide. RetL1, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nebritts, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy cassociated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome and cerebral palsy, or conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis). Fusion proteins are used to deliver toxins etc. to Ret-expressing collar, especially tumours.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; meningitis; myelopathy; Creutzfeldt-Jakob disea cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nerve cells
Claim 2; Page 49-51; 113pp; English.
Claim 2; Page 49-51; 113pp; English.
This protein comprises rat Ret ligand (RetL) RetLl, a key component of the Ret signalling pathway that specifically interacts with Ret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOJ ) BIOGEN INC.
Cate RL, Hession C,
WPI; 98-018431/02.
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08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
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27-NOV-1997.
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                       smsn-evcnrrkchkalrqffdkvpakhsygmlfcscr--diacterrrqtivpvcsyee
                                                                                                                                                                  XXXXXAXXECXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPY
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  XXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEX
                                                                                  Similarity
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ilarity 50.7%;
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                                                                                                                                                                                                                                                                                                                             Score 1779; DB 28;
Pred. No. 2.89e-167;
12; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                         Length 468;
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               PS Claim 2; Page 69-70; 113pp; English.
CLaim 2; Page 69-70; 113pp; English.
CC deduced from a cDNA clone (see V00248) isolated from a human foetal
CC deduced from a cDNA clone (see V00248) isolated from a human foetal
CC liver library. Rat and human RetLi, and human and mouse RetLi.3
CC RetL2 is 49.1% identical to human RetLi, and human RetLi is a
key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC vectors containing retL2 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL2, its soluble variants and
CC stated and the acxin, imageable compound or radionuclide.
CC RetL2, optionally when expressed from vectors in vivo, is used to
CC particularly kidney or neural tissue. Typical applications are in
CC considered with HIV or Creutzfeldt-Jakob disease, multiple sclerosis,
CC associated with HIV or Creutzfeldt-Jakob disease, multiple sclerosis,
CC seculated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Scauence 464 An.
CC secular, especially tumours.
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
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Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
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27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nerve cells
Claim 2; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ew nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cel rowth and improving survival of injured cells, especially renal or
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Length 464;

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Best Loc
Matches
Claim 1: Pages 91-93; 196pp; English.

The present sequence is the human glial cell line-derived neurotrophic factor (GDNF) receptor, which can be used to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally in combination with GDNF) glaucoma, retinal degeneration and hearing loss caused by injury to inner ear sensory neurons. The receptor can also be used to block stabilise GDNF activity, analyse GDNF related molecules and set in pharmaceutical formulations. Receptor expressing cells, preferably transfected ex vivo, can be used similarly by implantation, and the use of the receptor CDNA in gene therapy is
                                                                                                                                                                                                                                                                                                                                                                     Glial cell line derived neurotrophic factor receptor treat dopaminergic nerve cell disorders, e.g. Parkinson
                                                                                                                                                                                                                                                                                                                                                 treat dopaminergic r
Alzheimer's disease
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22-APR-1996; US-015907
09-MAY-1996; US-017221
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w35333 standard; Protein; 4
w35333;
01-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
FOX GM, Jing S, Wen D;
WPI; 97-535836/49.
N-PSDB; T88419.
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d. No. 3.90e-166;
Mismatches 187;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         also contemplated. Probes based on the cDNA can be used to identify GDNF responsive cells and tissues, e.g. to identify patients who would benefit from GDNF therapy, and abnormalities in receptor expression, and to isolate molecules that form a complex with the cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor antibodies, oligonucleotides derived from the cDNA and animal models that overexpress the receptor can be used to study the biological function of GDNF, knockout transgenic animals can be used to detect GDNF dependent neurons or processes and the antibody can be used in immunoassays for the receptor. The receptor binds CDNF specifically and with high affinity, acting as part of a complex that mediates/enhances signal transduction by GDNF, i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                            cisngnyekeglgasshittk-smaappscglspllvlvvtalstlls--ltets
pafpvqtttatttalrvknkp-lgpagsene1p-thvlppcanlqaqklksnvsgnthl
                                                                                                                          TPNYVDSXXTXXXVAPWCXCRGSGNXXEECEKFLXXFXXNPCLXNAIQAFGNGXDVXMSQ
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larity 49.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1695;
Pred. No. 1.
17; Mismatc
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1.23e-158;
tches 211;
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489
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27-NOV-1997.
07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Ret ligand RetLl.

Ret ligand; RetL; RetLl; receptor; signal transduction; Ret ligand; RetL; receptor; signal failure; neph cell growth; renal cell; nerve cell; renal failure; neph kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple scler infection; meningitis; myelopathy; Creutzfeld: Jakob discranial nerve injury; spinal cord injury; bown's syndrom cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9744356-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Claim 2; Page 64-66; ll3pp; English.
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                                       cisngnyekeglgasshittk-smaappscglspllvlvvtalstlls--ltets
                                                                                                                                                                                 tpnyidss-sls-vapwcdcsnsgndleeclkflnffkdntclknaiqafgngsdvtvwq
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                                                                            pafpvqtttatttalryknkp-lgpagseneip-thvlppcanlqaqklksnvsgnthl
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Pred. No. 2.11e-153;
17; Mismatches 206;
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Claim 2: Page 60-61; 113pp; English.

CC This amino acid sequence comprises a human Ret ligand (RetL) RetL1

CC partial polypeptide sequence, deduced from a partial clone (see

CC V00246) isolated from a human embryonic kidney cDNA library; a

CC full-length RetL1 sequence (see W37459) is also claimed, as well

CC as rat RetL1 and mouse and human RetL2 and RetL3 sequences (see

CC W37457 and W37460-63). Ret ligand is a key component of the Ret

CC signalling pathway that specifically interacts with Ret receptor

CC protein, triggering Ret dimerisation and/or autophosphorylation of

CC the Ret tyrosine kinase domain. Vectors containing retL1 DNA and

CC prokaryotic or eukaryotic host cells transformed or transfected

CC with these vectors are claimed, as well as a method for production

CC imageable compound or radionuclide. RetL1, optionally when

CC expressed from vectors in vivo, is used to promote growth of new

CC tissue and survival of damaged tissue, particularly kidney or

CC neural tissue. Typical applications are in renal failure,

CC neural tissue. Typical applications are in renal failure,

CC neural tissue. Typical applications are in renal failure,

CC neural tissue. Typical applications (e.g. multiple sclerosis,

Daterial, viral or prion infections (e.g. multiple sclerosis,

CC system (Lyme disease, muscular disorders such as Down's syndrom.

CC system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC ells, especially tumours.
                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel M;
WPI; 98-018431/02.
N-PSDB; V00246
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
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WO9744356-A2.
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                        vcsyeerekpnclnlqdscktnyicrsrladfftncqpesrsvssclkenyadcllaysq
                                                                                                 itpcttsvsn-dvcnrrkchkalrqffdkvpakhsygmlfcscr--diacterrrqtivp | ...
                                                                                                                                                            SCSYEXXEXPNCLDLRSXCRTDXLCRSRLADFXTNCXPXXRXXTXCXAXNYXXCLXAYXG
                                                                              IXXCXXXXSXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXI
                                                                                                                                                                                                                                                         similarity 51.0%;
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                                                                                                                                                                                                                                     Score 1255; DB 28;
Pred. No. 1.41e-113;
16; Mismatches 145;
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              PT nerve cells

CLaim 2: Page 77-78; 113pp; English.

CC Inim 2: Page 77-78; 113pp; English.

CC A this amino acid sequence comprises mouse Ret ligand (RetL) RetL3, deduced from cDNA clones (see v00249) isolated from an EST deduced from cDNA clones (see v00249) isolated from an EST deduced from cDNA clones (see v00249) isolated from an EST claimed. RetL1 and RetL3 cdatabase and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3 csequences (see W37457-60 and W37462-63) are also claimed. RetL is calculated to component of the Ret signalling pathway that specifically component of the Ret signalling pathway that specifically component of the Ret signalling pathway that specifically component of the Ret tyrosine kinase domain.

CC and/or autophosphorylation of the Ret tyrosine kinase domain.

CC vectors containing retL3 DNA and prokaryotic or eukaryotic host cells transformed or transfected with these vectors are claimed, as component of retL3, its soluble variants and compound for proteins with a toxin, imageable compound or radionuclide. CC well as a method for production of RetL3, its soluble variants and ccellar proteins with a toxin, imageable compound or radionuclide. CC particularly when expressed from vectors in vivo, is used to compound growth of new tissue and survival of damaged tissue, are in creal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, motor neurone disease, multiple sclerosis, associated with HIV or Creutzfeldt-Jakob disease, cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome can conditions involving the peripheral nervous system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC convences and the conditions involving the peripheral nervous cystem (Lyme disease, muscular dystrophy and myasthenia gravis).

CC convences and the conditions involving the peripheral nervous cystem (Lyme disease, muscular dystrophy and myasthenia gravis).
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10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Ret ligand RetL3.

Ret ligand; RetL; RetL3; receptor; signal transduction; mouse; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cel growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V00249
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27-NOV-1997.
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se 397 AA;
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Query Match Best Local

Similarity

46.78;

Score 976; Pred. No. 3

DB 28; .53e-85;

Length

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TRESULT
ACCORD
A
pr nerve cells
Claim 2; Page 85-86; 113pp; English.

Claim 3; Page 85-86; 113pp; English.

Claim 4; Page 85-86; 113pp; English.

Claim 4; Page 85-86; 113pp; English.

Claim 4; Page 85-86; 113pp; English.

Claim 5; Page 85-86; 113pp; English.

Claim 6; Page 85-
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08-MAY-1996;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O7-JUL-1996; US-UZIOJ.
(BIOJ) BIOGEN INC.
--- Pr. Hession C, Sanicola-Nadel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Ret ligand RetL3. "Ret ligand; RetL4; RetL3; receptor; signal transduction: human; Ret ligand; RetL5; RetL3; receptor; signal transduction: human; cell growth; renal cell; nerve cell; renal failure; nephrit1s; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningit1s; myelopath; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding ret receptor ligands and related proteins - vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
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WPI; 98-018431/02.
N-PSDB; V00251.
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W09744356-A2.
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US-017427.
US-017427.
US-019300.
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Best Local S
Matches 14
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W09744356-A2.

27-NOV-1997.

07-MAY-1997; U07726.

10-APR-1997; US-017427.

08-MAY-1996; US-017427.

07-JUN-1996; US-019300.

16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                       21-MAY-1998 (first entry)
Mouse Ret ligand retL3 partial sequence.
Ret ligand; RetL; RetL3; receptor; signal transduction; mouse; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Takob disease; cranial nerve injury; spinal cord injury; Down's syndrome; crarebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
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                                                  (BIOJ ) BIOGEN INC.
Cate RI, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
N-PSDB; V00256.
New nucleic acid encoding ret rece

    vectors,
    growth and

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transformed cells and antibodies, used for promount
improving survival of injured cells, especially
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1.29e-80;
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                              07-MAY-1997; U07726.
10-APR-1997; US-017427.
08-MAY-1996; US-017427.
07-JUN-1996; US-019300.
16-JUL-1996; US-021859.
                                                                                                                                                                                                                                                                                                                                                                                                              Human Ret ligand RetL3 partial sequence.
Ret ligand; RetL3; receptor; signal transduction; human cell growth; renal cell; nerve cell; renal failure; nephritis kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; bown's syndrome; cerebral palsy; Lyme disease; muscular dystrophy; myasthenia gravis; tumour; therapy.
Claim 2; Page 81-82; 113pp; English.

This amino acid sequence comprises a human Ret ligand (RetL) Retl partial polypeptide sequence, deduced from a partial clone (see V00250) isolated from a human adult heart cDNA library; a full-length RetL3 sequence (see W37463) is also claimed, as well as rat and human RetL1, human RetL2 and mouse RetL3 sequences (see W37455-61). Ret ligand is a key component of the Ret signalling pathway that specifically interacts with Ret receptor protein, triggering Ret dimerisation and/or autophosphorylation of
                                                                                                                                                                New nucleic acid encoding ret vectors, transformed cells growth and improving survival
                                                                                                                                                                                                                                (BIOJ ) BIOGEN INC.
Cate RL, Hession C, Sanicola-Nadel
WPI; 98-018431/02.
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l Similarity 45.2%;
127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 315
                                                                                                                                                                  survival of
                                                                                                                                                                ret receptor ligands and related proteins lls and antibodies, used for promoting cel val of injured cells, especially renal or
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Pred. No. 1.55e-73;
29; Mismatches 107
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Query Match
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region
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Cytotactin; neuron; neurite; cell attachment; cell elongation;
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                                                    region
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21-JUN-1996 (first entry)
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R94563 standard; Protein; 1810
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hes 126; Conser
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774..864
                              /note= "EGF-like repeat region"
592...773
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1..591
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 repeat VaVbVc"
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e- "fibronectin type III repeats I-II"
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                                                                                                   "fibronectin
                                                                                                                                    "fibronectin
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Pred. No. 2.81e-67;
34; Mismatches 135;
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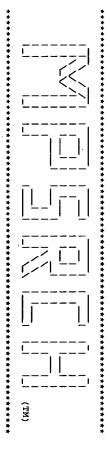
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Best Local s
Matches 2
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Chicken cytotactin (R94563) and human cytotactin (R94562) are
multidomain extracellular matrix proteins capable of simulating
neuronal cell attachment, neurite outgrowth and cell elongation.
The cytotactins, or functional portions of them (see R94564-69),
can be obtd. by expression of encoding DNA (see T14548 and
(T14547) in host cells, e.g. as GST fusion proteins in Escherichia
coli. They have therapeutic and diagnostic applns. and can he
                                                  modified_site
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Crossin KL, Phillips G,
WPI; 96-179904/18.
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14-SEP-1995; U11684.
16-SEP-1994; US-308359.
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Similarity 24.3%;
25; Conservative
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101
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812
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1570..1810
/note- "fibrinogen domain plus
III repeat VIII N-terminus"
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Pred. No. 7.44e+00;
18; Mismatches 49
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 8 15:04:28 1999; MasPar time 23.89 Seconds 766.704 Million cell updates/sec

Tabular output not generated.

Run on:

Title:
Description:
Perfect Score:

Sequence: >US-08-866-354-44
(1-48) from US08866354.pep
2092
1 XXXXXXXXXXPXXXXLXTLXS......PVLMLTXLXXXLXXXLXETS 489

Scoring table: PAM 150 Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 42.322; Variance 73.547; scale 0.575

SUMMARIES

20	Result No.	Score	Query Match	Length	BB	ID	Description	Pred. No.
	_	976	46.7	397	N	JE0082	GPI-linked receptor -	3.04e-198
	N	108	5.2	493	N	C562	growth f	.82e-0
	ω	109	5 2	2524	N	A35844	tein - A	6e
	4	108		3002	N	A47221	.lin 1 prec	2e-
	5	107		2871	N	A55567	н	
	σ	105		2871	N	A55624	fibrillin-1 precursor	.38e-
	7	96	4.6	387	N	I38449	extracellular protein	1.25e-01
	œ	96	4.6	1810	N	A32230	precu	56
	Q	94	4.5	570	N	A48836	fibropellin C precurs	2.44e-01
	10	94	4.5	879	_	QRRTLD	tor p	2.44e-01
	11	95	4.5	1232	N	D64413	О	1.75e-01
	12	94	4.5	1700	N	S08167	Balbiani ring 3 prote	2.44e-01
	13	95	4.5	2531	N	A46019	gene Notch-1 protein	1.75e-01
	14	94	4.5	2555	N	A40043	protein	2.44e-01
	15	92	4.4	259	N	S48713	fetal antigen 1 - hum	4.74e-01
	16	92	4.4	260	N	A44549		4.74e-01
	17	92	4.4	383	N	548	- 1	4.74e-01
	18	92	4.4	383	N	S53716	homeotic protein dlk	4.74e-01
	19	92	4.4	469	N	A56918	farnesoid x-activated	4.74e-01
	20	93	4.4	2703	N	A24420	notch protein - fruit	3.41e-01
	21	92	4.4	2907	N	A57278	fibrillin-2 precursor	4.74e-01
	22	92	4.4	2918	ν	A54105	111in-2	4.74e-01
	23	89	4.3	200	N	A26637	neurogenic repetitive	1.26e+00

4	4	4	4	41	4	ω	w	ω	ω	w	u	u	w	u	ω	2	2	2	2	N
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86	86	86	86	88	88	87	88	87	87	87	88	89	90	89	89	91	89	89	90	89
4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	۵.	۵.	4.3	4.3	<u>4</u> س	4.3	٠.3	4.	4.3
972	886	832	370	3069	2139	1251	1203	903	385	385	293	5147	3051	1712	854	826	603	511	427	385
2	N	N	N		N			N	N	N	N	μ.	N	N				N		
A30363	A57172	A31246	B43306	н70656	A35672	A57293	A49175	S60257	S53718	A54785	B26637	IJFFTM	S42373	A38261	QRHYLD	A60385	S28941	S44275	D64813	S68780
glycoprotein GP330, r	probable hormone rece	neurogenic protein De	DnrJ - Streptomyces p	probable fas protein	crumbs protein - frui	latent transforming g	Motch B protein - mou	meltrin alpha - mouse	homeotic protein dik	preadipocyte factor 1	neurogenic repetitive	cadherin-related tumo	hypothetical protein	masking protein precu	LDL receptor precurso	monocyte surface anti	coagulation factor XI	dopamine receptor pro	ybhC protein precurso	dopamine D1-like rece
3.26e+00	3.26e+00	3.26e+00	3.26e+00	1.73e+00	1.73e+00	2.38e+00	1.73e+00	2.38e+00	2.38e+00	2.38e+00	1.73e+00	1.26e+00	9.12e-01	1.26e+00	1.26e+00	6.59e-01	1.26e+00	1.26e+00	9.12e-01	1.26e+00

ALIGNMENTS

EACSGI-RCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPS		Db 181 Qy 190
DVSPYEDTVTSK-PWKM-NL-SKLNMLKPD-SDLCLKFAMLCTLHDKCDRLKKAYG		ob 129 Qy 130
RPLPLEESAMSA-DCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYFI :	70 RPLPLEESA 70 XNXXXXXXX	Qy 7
PLIMITLIVISLWIPIGAGNSLATENREVNSCTQARKKCEANPACKAAYQHLGSCTSSLS 6%	10 PLEMILLEV : 10 PXXXXLXTL	Qy J
46.7%; Score 976; DB 2; Length 397; ity 40.4%; Pred. No. 3.04e-198; nservative 35; Mismatches 157; Indels 19;	Query Match Best Local Similarity 40.4%; Matches 143; Conservative	Query Best I Matche
predicted #length 397 #molecular-weight 44307 #checksum 2962	#1	SUMMARY
#region hydrophobic\ #binding_site carbohydrate (Asn) (covalent) #status	380-397 92,145,306	380-3 92,14
_		FEATURE
T This protein plays a distinct role in cell survival and differentiation.	This prodiffer	COMMENT
	##residues 1-39	***
JE0082	ccession JE	#acce
MOLECULAr cloning and expression analysis of GFRalpha-3 novel cDNA related to GDNFRalpha and NTNRalpha.		#t1tle
Biochem. Biophys. Res. Commun. (1998) 244:849-853	al	#journal
Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.	rs	#authors
JE0082 JE0082	ខ	ACCESSIONS REFERENCE
<pre>#formal_name Mus musculus #common_name house mouse 21-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1998</pre>		ORGANISM DATE
GFRalpha-3	E_NAMES	ALTERNATE_NAMES
JECONZ. #Type complete	. C	ENTRY
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RESULT
ENTRY
TITLE
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1957-1989
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#title
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200-237,238-277,
278-318,319-359
                                                                                                                                                                                                                                                           #title Xotch, the Xenopus homolog of Drosophila notch.
#cross-references_MUID:90385285
                                                                                                                                                                                                                                                                                                                   #authors
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                                                                                                                                                                    ##molecule_type mRNA
##residues 1-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references DDBJ:D89730; NID:g2429082; PID:d1023127; PID:g2429083
This protein plays a role in the regulation of cell growth by
interacting with DAN protein through DA41 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 IGTAMTPNFISKVNTT--VALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAA 344
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                                                                                                                         1-2524 ##label COF
#Superfamily unassigned ankyrin repeat
repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                              A35844 #type complete

Xotch protein - African clawed frog
#formal_name Xenopus laevis #common_name African clawed frog
12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change
14-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; A.; Sakiyama, S.
Blochem. Blophys. Res. Commun. (1997) 237:245-250 Interaction of DA41, a DAN-binding protein, with tepidermal growth factor-like protein, S(1-5). JC5621
                                                                                                                transmembrane
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epidermal growth factor-like protein, T16 - rat
#formal_name Rattus norvegicus #common name No--
09-Oct-1997 #sequence rowing.
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#domain ankyrin repeat homology *label
                                                                         #domain EGF homology #label EGF\
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#binding_site carbohydrate (Asn) (covalent)
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l translation
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AN2/
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Best Local
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                                                                                                                                                                                   #title
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#journal Hum. Mol. Genet. (1993) 2:961-968
#title Genomic organization of the sequence coding for
the defective gene product in Margan syndrome
#cross-references MUID:93372860
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                                                    ##residues 2217-2288,'I',2290-2325 ##label RES ##cross references GB:S54426; NID:g264860; PID:g264861
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                                                                                     **Status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
                                                                                                                                                                                                                                                   ##cross-references EMBL:X63556
                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
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##residues 132-3002 ##label PER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##Status
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   Lee, B.; Godfrey, M.; Vitale, E.;
Sarfarazi, M.; Tsipouras, P.; Re
                                                                                                                                                        Dietz, H.C.; Valle, D.; Francomano, Science (1993) 259:680-683
The skipping of constitutive exons nonsense mutations.
                                                                                                                                                                                                                                                                                                                                      Maslen, C.L.; Corson, G.M.;
Sakai, L.Y.
Nature (1991) 352:334-337
                                         S17062
                                                                                                                                                                                                                                                                                                           Partial sequence of a candidate S17064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakai, L.Y.

Genomics (1993) 17:476-484

Fibrillin binds calcium and is coded by cDNAs that reveal multidomain structure and alternatively spliced exons at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Homo sapiens #common_name man 02-Jun-1995 #sequence_revision 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrillin 1 precursor - human (fragment)
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jth 2524 #molecular-weight 274931 #checks
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 Tsipouras,
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                                                                                                                                                                                                                                                                                                                                                                         Maddox, B.K.; Glanville,
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     Ramirez,
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Hori, H.; Mattel, M.G
amirez, F.; Hollister,
                                                                                                                                                                              in vivo
                                                                                                                                                                                                               C.A.; Kendzior,
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 8 15:07:33 1999; MasPar time 36.57 Seconds 737.616 Million cell updates/sec

Title: Description: Perfect Score: >US-08-866-354-44
(1-48) from US08866354.pep
2092
1 XXXXXXXXXXPXXXXLXTLXS......PVLMLTXLXXXLXXXLXETS 489

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb18

1:sp_archea 2:sp_bacter1a 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 42.421; Variance 67.360; scale 0.630

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	Ħ	Description	Pred. No.
-	1800	86.0	464	11	035977	GLIAL CELL LINE-DERIVE	0.00e+00
2	1768	84.5	464	4	015328	IGAND	0.00e+00
ω	1768	84.5	464	4	015316	GLIAL CELL LINE-DERIVE	0.00e+00
4	1762	84.2	468	11	035246	GDNF RECEPTOR ALPHA.	0.00e+00
G	1728	82.6	463	11	035748	GDNFR-ALPHA/TRNR1-DELT	0.00e+00
თ	1711		463	11	035252	GDNF RECEPTOR BETA.	0.00e+00
7	1695	81.0	465	4	043912	GPI-LINKED ANCHOR PROT	0.00e+00
œ	1644	78.6	460	4	015507	RET LIGAND 1.	0.00e+00
9	1244	59.5	431	13	093512	GFR RECEPTOR ALPHA 4 P	1.78e-287
10	976	46.7	397	11	035118	GLIAL CELL LINE DERIVE	6.99e-217
11	976	46.7	397	11	035325	GLIAL CELL LINE-DERIVE	6.99e-217
12	976	46.7	397	11	055243	GLIAL CELL LINE-DERIVE	6.99e-217
13.	928	44.4	400	٠	060609	GDNF FAMILY RECEPTOR A	2.57e-204
14	108	5.2	493	11	035568	T16.	6.98e-04
15	105	5.0	1523	11	088280	MEGF5.	2.28e-03
16	105	5.0	3857	11	088840	MUTANT FIBRILLIN-1.	2.28e-03
17	97	4.6	192	ű	001471	COSMID CO4E6.	4.80e-02
18	96	4.6	387	4	Q12805	EXTRACELLULAR PROTEIN	6.96e-02
19	97	4.6	752	13	042374	NOTCH RECEPTOR PROTEIN	4.80e-02
20	96	4.6	1062	11	Q60789	FIBRILLIN-2 (FRAGMENT)	6.96e-02

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NOTCH HOMOLOG SCALLOPE CODED FOR BY C. ELEGAN	156D SUFACE ANTIGEN.	RITY TO EG	LATENT TGF BETA BINDIN	220 KDA SILK PROTEIN.	REVERSE TRANSCRIPTASE.	COSMID F38E9.	METHIONINE SYNTHASE RE	OXALOACETATE DECARBOXY	FIBROPELLIN III (FRAGM	COSMID F07C4.	ALPHA-51D IMMOBILIZATI	ALPHA-51D-IMMOBILIZATI	NOTCH HOMOLOG.	×	PUTATIVE CYSTINE-RICH	FIBRILLIN (FRAGMENT).	FARNESOID X ACTIVATED	200 KD TENASCIN PRECUR	185 KDA SILK PROTEIN.	190 KD TENASCIN PRECUR	HYPOTHETICAL PROTEIN M	MEGF5 (FRAGMENT).	CYTOTACTIN 200KD PRECU
8.61e-01 4.26e-01	. 26e	4.26e-01	.61e	8.61e-01	8.61e-01	6.06e-0			8.61e-01	_			2.08e-01		2.98e-0	.08e-	.98e-	. 456	1.45e-01	. 45e	00e	.006	. 96€

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPINSKY R.B., CATE R.L.;

"Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";

PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).

EMBL; U97145; G2282038; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANICOLA M., HESSION C.A., WALUS L., ROBINSON S., JAW
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LIVER;
MEDLINE; 9732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
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                                                                                                                                                                                                                    ---ANKECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYE- 129
                        SPTERCNRRKCHKALRQEFDRVPSEYTYRMLFCSCQ--DQACAERRRQTILPSCSYEDKE
                                                                                                                    PVTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREI
                                                                                                                                                                                      XXXAXXECXXAXEXLXXSSLYDCRCKRGMKKEXXCLXIYWSXHXXLXXGXXXLEXSPYEX 136
                                                                                                                                                                                                                                                                                    TLXSLXXPLXLXXSXXXXXXXXXXXDCVXAXXXXCXAEXXCSXXYRTLRQCXAGXXXXXXXXXX 76
SXXERCNRRKCHKALRQFFDKVPXXHXYGMLFCSCXXXDXACXERRRQTIXPSCSYEXXE
                                                                                           PVTSRLSDIFRXXSXXXXXXXXXXXXXXXXXCLDAAKACNLNDXCKKLRSAYIXXCXXXX
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity 53.3%, 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866
                                                                                                                                                                                                                                                                                                                                                                                  Score 1768; DB 4;
Pred. No. 0.00e+00;
14; Mismatches 187;
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Best Local Similarity
Matches 244; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M., MOSHNYAKOV M., AIRAKSINEN M.S., PALOTIE A., SARTOLA H., SAARMA M.; SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U93703; G2228737; -.
SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
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EUKARYOTA; METAZOA; CHORDATA;
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                                                 TELTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLML 460
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SPTERCNERKCHKALRQFFDRVPSEYTYRMLFCSCQ--DQACAERRRQTILPSCSYEDKE
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                                                                                                     PSFQATQAP-----RVEKTPSLPDDLSDSTSLGTSVITTCTSVQEQGLKANNSKELSMCF 422
                                                                                                                                                                                                                                                                                                                        XPNCLDLRSXCRTDXLCRSRLADFXTNCXPXXRXXTXCXAXNYXXCLXAYXGLIGTXMTP
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ilarity 53.3%;
Conservative
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Pred. No. 0.00e+00;
14; Mismatches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA;
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01-JAN-1998 (TREMBLREL 05, CREATED)
01-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
101-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
101-JAN-1998 (TREMBLELL 05, LAST ANNOTATION UPDATE)
101-JAN-1998 (TREMBLELL 05, LAST ANNOTATION UPDATE)
101-JAN-1998 (TREMBLEL 05, LAST ANDOTATION UPDATE)
101-JAN-1998 (TREMBLEL 05, LAST ANDOTATION UPDATE)
101-JAN-1998 (TREMBLEL 05, LAST SEQUENCE UPDATE)
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O35246;
O1-JAN-1998 (TREMBLREL. C
O1-JAN-1998 (TREMBLREL. C
O1-JAN-1998 (TREMBLREL. C
GDNF RECEPTOR ALPHA.
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GDMRR-ALPHA.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; MUTIDAE; MURINAE; MUS.
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STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF014117; G2624961; *.
SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO
'NEUROREPORT 9:0-0(0001).
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Pred. No. 0.00e+00;
19; Mismatches 211
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Query Match
Best Local S
Matches 23
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Best Local S
Matches 24
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O35252;
O1-JAN-1998 (TREMBLREL. C
O1-JAN-1998 (TREMBLREL. C
O1-JAN-1998 (TREMBLREL. C
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*MUS MUSCULUS (MOUSE).

*EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;

*SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AJ002072; E1154274;
SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;
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                                                                                           DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF015172; G2624963; -.
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NEUROREPORT
                                                                                                                                                                                                                                                                                       DEY B.K.,
                                                                                                                                                                                                                                                                                                             STRAIN-C57;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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12; Mismatches 208;
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CATARRHINI; HOMINIDAE;
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Best Local S
Matches 23
                                                                                                                                                                 MEDLINE: 9732356.

SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO F., SANICOLA M., HESSION S., JAWORSKI G., WEI H., TIZARD R., WEINSKY R.B., CATE R.L.;
PEPINSKY R.B., CATE R.L.;
"Glial cell line-derived neurotrophic factor-dependent R can be mediated by two different cell-surface accessory NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ULT 8
015507 PRELIMINARY;
015507;
01-JAN-1998 (TREMBLREL. (
01-JAN-1998 (TREMBLREL. (
01-NOV-1998 (TREMBLREL. (
                                                        SANICOLA M., HESSION C.A., WORLEY D. WALUS L., ROBINSON S., JAWORSKI G., PEPINSKY R.B., CATE R.L.; SUBMITTED (APR-1997) TO EMBL/GENBANI
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TISSUE-SUBSTANTIA
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TISSUE-KIDNEY;
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EUKARYOTA; METAZOA; CHORDATA;
                   SEQUENCE FROM N.A
                                                                                                                                               TISSUE-KIDNEY;
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EMBL; AF058997; G3068783;
EMBL; AF058998; G3068783;
SEQUENCE 465 AA; 51455
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235; Conservative
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NIGRA;
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                                                          EMBL/GENBANK/DDBJ
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Pred. No. 0.00e+00;
17; Mismatches 211
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H., TIZARD
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